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June 6, 2004, 10:01:11; Search time 2267 Seconds (without alignments) 5965.164 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1 AY040564 LOCUS	AY040564 461 bp mRNA linear PRI 15-AUG-2001	01
DEFINITION	Homo sapiens Hin-1 putative cycokine mkna, compiere cus. AY040564	
VERSION	AY040564.1 GI:15079187	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	
	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 461)	
AUTHORS	<pre>Krop,I.E., Sgroi,D., Porter,D.A., Lunetta,K.L., LeVangie,R.,</pre>	
	Seth, P., Kaelin, C.M., Rhei, E., Bosenberg, M., Schnitt, S.,	
	Marks, J.R., Pagon, Z., Belina, D., Razumovic, J. and Polyak, K.	

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JOURNAL
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/product="HIN-1 putative_cytokine"
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/translation="WKLAALGGCVALSCSSARAFLVGSAKPVAQPVAALESAAEAGA
GTLANPLGTLNPLKILLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV
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1 (bases 1 to 461)
Clippe, A., Laing, I.A., LeSouef, P.N., Bernard, A. and Knoops, B. Molecular cloning of PnSP-1, a protein of the respiratory tract with potential association to atopy
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HIN-1, a putative cytokine highly expressed in normal but cancerous mammary epithelial cells
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9796-9801 (2001)
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/note="high in normal-1 putative cytokine"
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100.0%; Pred. No. 1.9e-39;
tive 0; Mismatches 0;
                                                                                   Delyak,K., Krop,I. and Sgroi,D.
Polyak,K., Krop,I. and Sgroi,D.
Direct Submission
Submitted: [15-JUN-2001] Adult Oncology, Institute, 44 Binney St. D740C, Boston, Location/Qualifiers
                                                                                                                                                                                    1. .461
/organiam="Homo sapiens"
/mol_type="mRNA"
/db zref="taxon:9606"
/chromosome="5"
/map="5335-tel"
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2 (bases 1 to 461)
Clippe,A., Bernard,A. and Knoops,B.
Direct Submission
Submitted (22-00T-2201) Unit of Toxicology, Catholic University of Louvain, Clos Chapelle-aux-Champs, 30.54, Brussels, B 1200, Belgium Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens full length insert cDNA clone ZB52D10.
AF086152
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Acorganism="Homo sapiens"
(mcl_type="mRNR"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                           /codon_start=1
/product="pneumo
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Homo sapiens (human)
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gene="SCGB3A1"
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                Waterston,R.
Direct Submission
Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC029176

Homo sapiens secretoglobin, family 3A, member 1, mRNA (cDNA clone MGC:34758 IMAGE:5180304), complete cds.
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                                                                                                                                                                                                                                            NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence accross the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted
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/clone_lib="Soares_fetal_lung_NbHL19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                            Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu
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1, .471
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REMERYOR PRESENCE TO COLORIAN CATCHER, CATCHER,
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A61K37/02,C12N5/00
Incyte Clone No: 3120415
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UP 2002519030-A/65.
Homo sapiens (human)
                                99.0%;
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Best Local Similarity
Matches 310; Conserv
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Strandedness: Single;
Topology: Linear;
Key Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1998 JP 1998533078
31-JAN-1997 US 08/791710
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
/translation="MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA
GTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV
FG"
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(Dases 1 to 519)

Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Mcdel, P.A.B., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R. Russell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the lung habort laborators:

Patent: JP 200122225-A 6 13-NOV-2001;

Phy JP 200152225-A/6

Phy 13-NOV-2001
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN
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                                                                           Score 308.8; DB 9;
Pred. No. 5.9e-39;
0; Mismatches 2;
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/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
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                                                                               Query Match
Best Local Similarity 99.4
Matches 310; Conservative
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PN JP 2002519030-A/65

PD 02-JUL-2002

PP 25-JUN-1999 UP 2000557363

PR 26-JUN-1999 US 60/099762,31-JUL-1998 US 60/194983 PR

26-JUN-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREFIT

1-AL, Y TOW TAMO, GINA A CONGONE, NEIL C CORLEY, KARL J PI GUBGLER,

PI MARIAH R BAUGHN INCRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,

PI CHANDRA PATTERSON, ROOPA, REDDY, JENNIFER L HILLMAN, OLGA BANDMAN PC C12N15/09, AGIK38/00, AGIK39/395, AGIK45/00, AGIR9/00, AGIR15/00,
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I (bases I to 53.

Ial, P., Tang, Y. T., Gorgone, G. A., Corley, N. C., Guegler, K. J., Baughn, M. R., Akerblom, I. E., Young, J. A., Yue, H., Patterson, C., Human signal peptide-containing protein

Patent: JP 200219030-A 65 02-JUL-2002,

INCYTE FHARMACEUTICALS INC
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Location/Qualifiers
1. :543
/organism="Homo sapiens"
/mol_type="genomic DNA"
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Score 308.8; DB 6;
Pred. No. 5.8e-39;
); Mismatches 2;
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DEFINITION

RESULT 7 BD226775

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ORGANISM

KEYWORDS SOURCE

VERSION

AUTHORS TITLE JOURNAL REFERENCE

COMMENT

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BDO82141 Set by DNA linear PAT 27-AUG-2002 Reagents and methods useful for detecting diseases of the lung. BDO82141
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Strandedness: Single; Topology: Linear;
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Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D.
Russell, J.C. and methods useful for detecting diseases of the lung Patent: JP 2011522225-A 5 13-NOV-2001;
ABBOTT LABORATORIES
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PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITIS, PAULA
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93 AIGAAGCICGCCCCCCCCCGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCTGCT
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                   JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
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/db_xref="taxon:4577"
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31-JAN-1997 US 08/7917
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/organism="Zea mays"
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JP 2001522225-A/5.
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13-NOV-2001
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A novel method of diagnosing, monitoring and staging lung cancer.
BD226775
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
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                                                                                      Length 543;
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C12N15/09, C12Q1/68, G01N33/50, C12N15/00
A novel method of diagnosing, monitoring
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99.4%; Pred. No. 5.8e-39;
iive 0; Mismatches 2;
                                                                                Score 308.8; DB 6;
Pred. No. 5.8e-39;
0; Mismatches 2;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 202515262-A/6
28-NAY-2002
12-MAY-1999 JP 2000549766
21-MAY-1999 US 60/086212
/db xref="taxon:9606"
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JP 2002515262-A/6.
Homo sapiens (human)
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                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.

1 (bases 1 to 570)

Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.

Implant, method of making same and use of the implant for the treatment of bone defects
Patent: US 6478825-A 407 12-NOV-2002;

Location/Qualifiers
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Pred. No. 5.7e-39;
0; Mismatches 2;
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Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
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US 6478825.
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                    AR252648
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Compositions and methods for the treatment of tumour Patent: WO 0151486-A 27 26-JUL-2001;
Genentech, Inc. (US)
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Direct Submission
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Matches 310; Conserv
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1 (bases 1 to 570)

2 (lark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Liewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yannsura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Biffort to Identify Novel Human Secreted and Transmembrane Proteins:
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Submitted (01-3405-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA WAY, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                  ATGAAGCTCGCCGCCCTCCTGGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCCTGCTGCT
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                                                                                                  Length 570;
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Homo sapiens clone DNA64884 SCGB3Al (UNG629) mRNA,
AY359064
                                                                                                                                   Indels
                                                                                                  Score 308.8; DB 6;
Pred. No. 5.7e-39;
0; Mismatches 2;
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                                  /mol_type="unassigned DNA"
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/organism="Homo sapiens"
                  'organism="Homo sapiens"
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/clone="DNA64884"
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Best Local Similarity 99.4%;
Matches 310; Conservative
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Homo sapiens (human)
Homo sapiens
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SOURCE

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2 (bases 1 to 347)
Nihmi,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A., Srisodsai,A.,
Zimonjic,D.B., Keck-Waggoner,C.L., Popescu,N.C. and Kimura,S.
Cloning, expression, and chromosomal localization of the mouse gene
(Scg55al, alias Ugrp2) that encodes a member of the novel
uteroglobin-related protein gene family
Cytogenet. Genome Res. 97 (1-2), 120-127 (2002)
                                                                                     /protein_id="AAQB9423.1"
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/translation="MKLAALIGLCVALSCSSAAAFLVGSAKPVAQPVKALKALIGALTV
FG"
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Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 347)
Niim,T., Keck-Waggoner,C.L., Popescu,N.C., Zhou,Y., Levitt,R.C.
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Pred. No. 5.7e-39;
0; Mismatches 2;
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/locus_tag="UNQ629"
/note="PR01245"
                                                                             /product="SCGB3A1"
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                                                   /codon_start=1
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ilarity 99.4%;
Conservative
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Homo sapiens
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/ codon start=1
/product="UGRP2"
/product="UGRP2"
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/translation="MKLAALGCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA
/translation="MKLASLGTCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA
/Translation="MKLASLGSRGTPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTV
PG"
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Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
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Submitted (25-JAN-2002) Froduction Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
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Submitted (16-OCT-2000) Laboratory of Metabolism, National Cancer Institute, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AC108083.1 GI:18369929
HTG: PHTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HTmo sapiens (human)
Home sapiens
                                                                                                                                                                                                                                                                                                            DB 9;
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س
                                                                                                                                                                                                                                                                                                          Score 307.2; DB 9;
Pred. No. 1.1e-38;
0; Mismatches 3;
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/organism="Homo sapiens"
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11.325
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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99.0%;
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Matches 309; Conservative
                                                      .347
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AC108083
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KEYWORDS
SOURCE
                                     FEATURES
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166777 bp DNA linear HTG 07-MAR-2002

Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; am-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49334 CAGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49454 TGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCAACCCTCAACCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the accession number will
                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wilbe preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 130129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4320: contig of 4320 bp in length 4420: gap of unknown length 23712: contig of 19292 bp in length 23812: gap of unknown length 48602: contig of 24790 bp in length 48702: gap of unknown length 130129: contig of 81427 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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AC106813.3 GI:19224876
HTG: HTGS PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
Home sapiens (human)
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Pred. No. 1.9e-28;
0; Mismatches 3;
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1. 130129
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Center Project Name: 632820
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Best Local Similarity 98.8%;
Matches 240; Conservative
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Sequencing of Human Chromosome 5 Unpublished

TITLE

REFERENCE

1 (bases 1 to 166777) DOE Joint Genome Institute.

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Consensus quality: 166429 bases at least Q40
Consensus quality: 166071 bases at least Q30
Consensus quality: 166071 bases at least Q30
Consensus quality: 166432 bases at least Q30
Consensus quality: 166432 bases settleation
Estimated insert size: 16657; sum-of-contigs estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have

* This sequence will be replaced

* by the finished sequence as soon as it is available and

the accession number will be preserved.

* 62237: contig of 62237 bp in length
6238 75937: gap of unknown length

* 75938 15937: contig of 19300 bp in length
75938 15937: gap of unknown length

* 75938 16777: contig of funknown length
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                                                        Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases i to 166777)
DOE Joint Genome Institute.
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                                                                                                                                                                                                        Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 7, 2002 this sequence version replaced gi:18369924.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.jgi.doe.gov
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Center: Joint Genome Institute
Center Code: JGI
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Center Project Name: 1519801
   2 (bases 1 to 166777)
DOE Joint Genome Institute.
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Matches 240; Conservative
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REFERENCE
AUTHORS
TITLE
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Db 120440 AGTGTGGCTGGGTCCCCAGGCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGC 120499

Qy 290 TGG 292

Db 120500 TGG 120502

Search completed: June 6, 2004, 14:59:41
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GenCore version 5.1.6
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IDENTITY NUC Gapop 10.0 Gapop 10.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

genesegn2001as:* genesegn2001bs:* geneseqn2002s:* geneseqn2003as:* N_Geneseq_29Jan04:* geneseqn2003bs:* geneseqn2003cs:* genesegn1980s:* genesegn1990s:* geneseqn2000s:* 4.0.07 .. 6 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2004s:*

		Description	Aav54621 LU105 pol		Aaz98173 Human siq	6 Human	Aav54620 LU105 spe	Abk40267 cDNA enco	Aaz65103 Membrane-	Aaf44249 Human PRO	Abx77974 Human PRO		Aca69292 Human cDN	Human	CDNA e		Abx80890 Human sec	Acd44399 cDNA enco	Abx79570 Human sec		Abx81273 Novel hum		Abx17173 Human PRO	8 Novel	Aca88477 Human sec
SUMMARIES		QH.		AAZ29723	AAZ98173	ADE39936	AAV54620	ABK40267	AAZ65103	AAF44249	ABX77974	ABX80386	ACA69292	ABX90363	ABX64209	ACA64431	ABX80890	ACD44399	ABX79570	ACA93591	ABX81273	ACA93089	ABX17173	ACA68028	ACA88477
		DB	N	m	m	σ	C	9	m	Ŋ	7	۲-	7	7	7	7	7	7	۲-	7	7	7	7	œ	æ
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		Score	08.		308.8	08.		08.	08.	08.	308.8	08.		08.	08.	308.8	308.8		08.	08.	08.	08.	08	308.8	0.8
	Result	No.	Н	2	е	4	τU	v	7	œ	60	10	11	12	13	14		16	17	18	19	20	21	22	23

Acd81984 cDNA enco	Ada37918 Human cDN	Ada21604 Human cDN	Ada10391 Human cDN	Ada17935 cDNA enco	Ada28043 Human cDN		Ada38848 Human cDN	Ada92969 Human cDN	Ach65545 Human cDN	Ada22530 Human cDN		Ada06696 Human sec	Ada39389 Human cDN	Human	Human		Adc12118 Human cDN		Adc07595 Human cDN	Adc11585 Human cDN	Adc14707 Novel hum
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99.0	6	6	6	6	0.66	σ	9	σ,	φ,	99.0	σ.	0.66	99.0	φ,	φ.	σ,	ď,	σ,	σ.	0.66	σ,
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ALIGNMENTS

LU105; lung disease marker; immunoassay; lung disease; cancer; blood; plasma; serum; ss. LU105 polypeptide encoding cDNA clone 1327836IH AAV54621 standard; cDNA; 519 BP. (first entry) (revised) 25-MAR-2003 30-OCT-1998 AAV54621; RESULT 1
AAV54621
ID AAV5

Location/Qualifiers Homo sapiens.

/*tag= a /transl_except= (pos:136. .138, aa:Val) /product= "LUI05 polypeptide" WO9833926-A1 06-AUG-1998. Key

98WO-US001766. 97US-00791710.

30-JAN-1998; 31-JAN-1997; (ABBO) ABBOTT LAB.

Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J; Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrapp L; Russell JC, Stroupe SD;

WPI; 1998-437479/37. P-PSDB; AAW75868.

New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer.

Claim 11; Fig 1; 123pp; English.

Sequences shown in AAV54616 to AAV54621 represent LU105 specific

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contracted sequences. These are used in the method of the invention for detecting target LUIOS nucleic acid. The method comprises treating a sample with at least one LUIOS specific nucleic acid, or its complement which is at least 50 percent identical with the LUIOS specific nucleic acid sequences (AAVS4616 to AAVS4621). LUIOS is a lung disease marker. Cells transformed with a recombinant expression system that contains LUIOS specific nucleic acid fragments, are used to express recombinant LUIOS polypeptides which are used to raise antibodies. The antibodies are used to detect the LUIOS antigen, and correspondingly this antigen is used to detect the LUIOS antigen, in usual immunoassays. The LUIOS polypeptides and nucleic acid sequences are used for diagnosis, staging, nonitoring, prognosis, prevention, treatment and determination of susceptibility to, lung disease, specifically cancer. The LUIOS collection in altered form or lung disease (present at high concentration, in altered form or in an unusual body compartment). LUIOS can be detected in blood, plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%; Score 308.8; DB 2; Length 519; larity 99.4%; Pred. No. 4.3e-53; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
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Matches 310; Conserv
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GAGCTGGGGTCCCCCAGGCCGTGGGGCCCTGAAGGCCCTGTGGGCCCTGCTGGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                     diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antisthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; actological disorder; cirrhosis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Altheimer's disease; schbrenia; perimanel disorder; attentios disease; huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                       lungs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                               The present sequence is a lung specific gene (LSG) Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lurand is overexpressed in cancerous tissues. The sequence serves as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human signal peptide containing protein HSPP-65 cDNA SEQ ID NO:199
                                                                                                                                                                                                             A new method for diagnosing, monitoring and staging lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 308.8; DB 3; Length 543;
Pred. No. 4.3e-53;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                              Claim 6; Page 36; 40pp; English
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                  99WO-US010344
                                                   98US-0086212P
                                                                                                                       Sun Y;
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                                                                                      (DIAD-) DIADEXUS LLC
                                                                                                                         Macina RA,
                                                                                                                                                      WPI; 2000-116320/10.
P-PSDB; AAY44458.
                  12-MAY-1999;
                                                 21-MAY-1998;
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                                                                                                                       Yang F,
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120 152

212 180 272 240 332 300 332 300 392

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human signal peptide-contraining proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, curving correctives, cardiovascular and antiaschmatic activities, and can be used in gene therapy. HSPPs can be used to rreat or prevent disorders associated with increased activity or function of HSPP. Antagonists of mSPP associated with increased activity or function of HSPP. Antagonists of associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cirrhosis, psoriasis, acquired immune deficiency syndrom, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or schame, cheart disease, microbial or other infections, congestive or ischamen, cheart disease, Alzheimer's, Parkinson's or Huntington's diseases, Schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and amplification assays or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists, in related diseases (in usual immunoassays), as therapeutic antagonists, in related diseases (in usual immunoassays), as therapeutic antagonists, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                        Baughn MR;
t, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGGTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human signal peptide-containing proteins useful in treatment
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                                                                                                                                                                                                                                                                                                                                                                                     Corley NC, Guegler KJ, Ba
H, Patterson C, Reddy R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.8; DB 3;
Pred. No. 4.3e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 289; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        GA,
Yue 1
                                                                                                                                                                                                     98US-0094983P.
                                                                                                                  99WO-US014484
                                                                                                                                                                            98US-0090762P
                                                                                                                                                                                                                                                                98US-0112129P
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Best Local Similarity 99.04%;
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Gorgone
                                                                                                                                                                                                                                                                                                                                                                                                                 Au-Young J,
                                                                                                                                                                                                                                                                                                                          INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-160673/14.
P-PSDB; AAY87288.
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WO20000610-A2
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                                                                                                                                                                                                  31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
                                                                                                                  25-JUN-1999;
                                                                                                                                                                            26-JUN-1998;
                                                       06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                 Akerblom
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                                                                                                                                                                                                                                                                                                                                                                                     Lal P,
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The invention relates to a novel isolated cDNA and a cDNA encoding pepsin C. The polynucleotide of the invention may be useful as a probe or a component within an expression vector, as a diagnostic in assessing the prognosis and treatment of a lung disorder and as a potential therapeutic or target for the identification of therapeutics for lung disorders. Furthermore, the polynucleotide may be used to produce purified proteins or peptides which can subsequently be used to produce antibodies. The current sequence is that of the human lung disorder-related cDNA (SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 TICTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 236
CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cDNAs co-expressed with lung surfactant and surfactant synthesis genes, useful as diagnostics in assessing the prognosis and treatment a lung disorder, or as potential targets for identifying therapeutics
                                               GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTTGAAGGCCCTTGAAGGCCCTG
                                                                          GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTTAGTGGGCTCGGCCCAAGCCTGTGGCCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 561 BP; 86 A; 200 C; 189 G; 86 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 308.8; DB 9;
Pred. No. 4.3e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                        Human lung disorder-related cDNA - SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 6; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murry LE;
                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                      pepsin C; lung disorder; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                               ADE39936 standard; cDNA; 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2002; 2002US-00237435.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                         312
                                                                                                                                    ACAGIGITIGGC 404
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                                                                                                         ACAGTGTTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-810982/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung disorder
ng disorders.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                           29-JAN-2004
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                                                                           333 (
                                                                                                                                    393
                 273
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                                                                                                                                                                                                                                               ADE39936;
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                  Homo sapiens.
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                                                                                                                             GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300
GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG 296
                                                                                  CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCT
                                         CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease marker; immunoassay; lung disease; cancer; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
Hodges SC, Klass MR, Kratochvil JD, Robertsrapp L,
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of disease, specifically cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/transl_except= (pos:176. .178, aa:Val)
/product= "LU105 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUI05 specific consensus polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        AAV54620 standard; cDNA; 562 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 1; 123pp; English.
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                                                                                                                                                                                                                    ACAGIGITIGGC 312
                                                                                                                                                                                                                                                             ACAGIGITÍTGGC 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma; serum; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
30-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1998
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                                                                                  297
                                                                                                                             241
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAV54620;
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AAV54620
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susceptibility to, lung disease, specifically cancer. The LU105 polypeptides are also used to screen for specific binding agents, useful therapeutically. LU105 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment). LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICTTAGEGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                             6.0
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                                                                                                                                                                                                                                                                                                                                                                       1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
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                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                         99.0%; Score 308.8; DB 2; Length 562; 99.4%; Pred. No. 4.3e-53;
                                                                                                                                                                                                                                                                                   Pred. No. 4.3e-53;
0; Mismatches 2; Indels
                                                                                                                                                                                                  Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding human PRO1245 polypeptide.
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99US-0123972P.
99US-0133459P.
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99US-0140650P.
99US-0140653P.
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99US-0146222P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ACAGTGTTTGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 ACAGTGTTTGGC 433
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                   Local Similarity
hes 310; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200153486-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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11-MAR-1999;
11-MAY-1999;
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01-SEP-1999;
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, 4991-NUT-22
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Matches
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pharmaceutical; receptor immunoadhesin; gene mapping; ss.
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9805-0088028P

9805-0088028P
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98US-0087759P.
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98US-0090254P

98US-0090254P

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98US-0090444P

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98US-0089600P.
98US-0089653P.
                                                                                             99WO-US012252
                           Homo sapiens.
                                                WO9963088-A2
                                                                                           02-JUN-1999;
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24-JUN-1998;
24-JUN-1998;
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    polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene thorapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTGGGTCCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGCGGGGCCCTG 378
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                                                                                                                                                                       for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCCATAGAGGGCTCCCAGAAGTGTGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                      present invention relates to the isolation of novel human PRO
                                                                                                                                                                 Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                          Hillan KJ;
Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                         Length 569;
                                                                                                                                                                                                                                                                                                                                                 Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                       99.0%; Score 308.8; DB 6; Length larity 99.4%; Pred. No. 4.3e-53; Conservative 0; Mismatches 2; Indels
                                                                                          Gurney AL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane-bound protein PRO1245 encoding cDNA.
                                                                                         Goddard A, Godowski PJ,
Pan J, Pitti RM, Roy MA,
                                                                                                                                                                                                               Claim 50; Fig 27; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ65103 standard; cDNA; 570 BP
 99WO-US021090.
99WO-US028313.
99WO-US028301.
99WO-US028634.
                                01-DEC-1999; 99WO-US028634
05-JAN-2000; 2000WO-US000219
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                                                                                                  Pan J, F
Wood WI;
                                                                 (GETH ) GENENTECH INC.
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                                                                                                                                    2002-205567/26.
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Best Local Similarity
Matches 310; Conserv
                                                                                                                                  WPI; 2002-205567/
P-PSDB; AAU86141
                                                                                        Ashkenazi AJ,
15-SEP-1999;
30-NOV-1999;
                                                                                                  Marsters SA,
Watanabe CK,
                        01-DEC-1999;
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9805-0091978P

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98US-0097141P.
98US-0090540P-
98US-0090557P-
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98US-0090691P-
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98US-0090694P-
98US-0090695P-
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98US-0090863P.
98US-0091358P.
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98US-0091478P.
98US-0091486P.
98US-0091519P.
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                                 25-JUN-1998;
25-JUN-1998;
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240
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                                                                                                                                                                                                                                 The invention provides membrane-bound PRO polypeptides and polymucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have bomology with proteins including LDL receptors, The Ilgands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents. Receptor receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNN. PRO nucleic acid sequences also be useful for the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTTGCTGGGGGCCCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing; diagnostic assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 TICTIAGIGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ITCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGCGAGTCGGCGGCG
                                                      Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PR01245 (UNQ629) nucleotide sequence SEQ ID NO:407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 308.8; DB 3; Length Pred. No. 4.3e-53; 0; Mismatches 2; Indels
                                                                                                                                                               Membrane-bound proteins and related nucleotide sequences
                                                    Smith V,
                                                      Gurney AL,
                                                                                                                                                                                                    Claim 2; Fig 289; 822pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF44249 standard; cDNA; 570 BP.
                                                      Goddard A,
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Best Local Similarity 99.4%;
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant techniques
                 (GETH ) GENENTECH INC.
                                                                                                           WPI; 2000-072883/06.
                                                    Chen J,
Yuan J;
                                                                                                                            P-PSDB; AAY66757
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                                                  Baker K,
Wood WI,
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Jun

Wed

Homo sapiens

99US-0144758P 99US-0145698P. 99US-0146222P. 99US-0149396P. 99WO-US021090.

99WO-US021547. 99US-0158663P.

99WO-US028313 99WO-US028301

99WO-US030095.

05-JAN-2000; 2000WO-US000219. 06-JAN-2000; 2000WO-US000376. 11-FEB-2000; 2000WO-US003565. 18-FEB-2000; 2000WO-US0044341. 22-FEB-2000; 2000WO-US0044141. 2000WO-US004914. 2000WO-US005004. 2000WO-US005841. 2000WO-US006884. 2000WO-US008439 (GETH) GENENTECH INC. WO200073454-A1 Ashkenazi AJ, 24-FEB-2000; 30-MAR-2000; 01-DEC-1999; 16-DEC-1999; 20-DEC-1999; 26-JUL-1999; 28-JUL-1999; 15-SEP-1999; 08-OCT-1999; 30-NOV-1999 07-DEC-2000 Roy MA, Zhang Z; Claim

KP, Botstein D, Desnoyers L, Eaton Gerber H, Gerritsen ME, Goddard A, AL, Kijavin IJ, Napier MA, Pan J, Tumas D, Watanabe CK, Williams PM, Ferrara N, Fong S, Gerbe Grimaldi CJ, Gurney AL, Roy MA, Stewart TA, Tum Baker KP,

Godowski PJ;

Eaton

Paoni NF; Wood WI;

WPI; 2001-032160/04. P-PSDB; AAB65280.

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.

2; Fig 289; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can radiolabels or attribodies, that cause cell death. PRO nucleotide radiolabels or attribodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4470 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44687 to AAF46300 represent human PRO Polynucleotide and protein sequences given in the exemplification of the present invention

Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

1 ATGAAGCTCGCCCCCCCCCGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCGCGCTCGTGCT

99.0%; Score 308.8; DB 5; Length 570; 99.4%; Pred. No. 4.3e-53; ive 0; Mismatches 2; Indels 0;

Matches 310; Conservative

Query Match Best Local Similarity

Gaps

09-JUN-1998

120 198 180 258 240 318 79 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCTGCT 138 GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGCTGGGGGCCCTG 300 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG Human; PRO; gene; ss; cytostatic; tumcur; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy. GAGGCCGGGGCCCGTGGCCAACCCCTCGGCACCCTCAACCCGGTGAAGCTCTG GAGGCCGGGGCCCGGGCCTGGCCAACCCCTCGGCACCTCTAACCCCGCTGAAGCTCCTG 259 CTGAGCAGCCTGGGCCATCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGGCT CTGAGCAGCCTGGGCATCCCCGTGAACCACCACATAGAGGGCTCCCAGAAGTGTGTGGCT BP. 97US-0049787P.
97WS-0062250P.
97WS-0065186P.
97US-0065111P.
97US-0065111P.
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98US-0088028P. Human PRO polynucleotide #127 ABX77974 standard; cDNA; 570 2001US-00997666 14-APR-2003 (first entry) ACAGTGTTTGGC 312 ACAGTGTTTGGC 390 US2003027163-A1. 20-MAR-1998; 28-APR-1998; 07-MAY-1998; 28-MAY-1998; Homo sapiens 15-NOV-2001; 04-JUN-1998; 04-JUN-1998; 04-JUN-1998; -JUN-1998; 1997 24-NOV-1997 25-FEB-1998 04-JUN-1998 06-FEB-2003 16-JUN-1997 1997 NOV-1997 02-JUN-1998 ABX77974; 121 199 319 301 181 241 379 RESULT 9 ò qq δ g δ g à g à g A CONTRACTOR OF THE CONTRACTOR

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                                                                        99.0%; Score 308.8; DB 7; larity 99.4%; Pred. No. 4.3e-53; Conservative 0; Mismatches 2;
23-JUN-2000; 2000US-0213637P.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US023531.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WS-US03328.
07-SEP-2000; 2000US-0230978P.
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139 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGGG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stimulated T-1ymphocytes and are therapeutically useful for enhancing immune response. PR0928, PR0926, PR01068 or PR01132 enhance survival of retinal neurons coels (PR01132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PR0819, PR0813 and PR011066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PR01310, PR0844, PR01312, PR01192 and PR01887 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PR0 protein polynucleotide
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Godowski PJ;
Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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Berratas M, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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0; Mismatches 2;
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                                                                                                                                                                               2001WO-US019692
2001WO-US021066.
2001WO-US021735.
2001US-00941992.
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2000WO-US023522
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Matches 310; Conservative
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29-UN-2001;
29-UN-2001;
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23-AUG-2000;
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GAGGCCGGGGCCCCTGGCCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG
                                                                                                                                            GAGCTGGGTCCCCAGGCCGTGGAGGCCCTGAAGGCCCTGAAGGCCCTGCGGGGCCCTG
                                                                                               Human cDNA encoding secreted/transmembrane protein PRO1245.
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8US-0088738P 8US-00887428 8US-00881424 8US-0088824P 8US-0088824P 8US-0088818 8US-00888108 8US-0088108 8US-0089118P 8US-0089538P 8US-0089538P 8US-0089538P 8US-0089538P 8US-0089538P 8US-0089538P	9805-0089904F. 9805-0089908P. 9805-0089952P. 9805-0089952P. 9805-0090245F. 9805-0090244P. 9805-0090444P. 9805-00904444P. 9805-00904444P. 9805-00904444P. 9805-00904444P. 9805-00904444P. 9805-00904444P. 9805-0090442P. 9805-0090678P. 9805-0090678P. 9805-0090678P. 9805-0090678P. 9805-0090678P.	UXS-0091633E 3135-0091646E 3135-0091978E 3135-0091932E 3135-0091932E 3135-00913339E 8135-0092473E 8135-0092473E 8135-00924339E 8135-00924338 8135-00924338 8135-00924338 8135-0093331E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E 8135-0093312E
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11-AUG-1998; 12-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998; 26-AUG-1998; 27-AUG-1998; 27-AUG-1998; 28-AUG-1998; 28-AUG-1998; 28-AUG-1998; 28-AUG-1998; 28-AUG-1998; 28-AUG-1998; 27-AUG-1998; 28-AUG-1998; 2000WO-US008439. 2000WO-US013358. 2000WO-US013705. 2000WO-US014941. 2000WO-US015264. 2000WS-US015564.

22-DEC-1999 05-DAN-1999 12-MAN-1999 12-MAN-1999 12-MAN-1999 12-MAN-1999 12-MAN-1999 10-MAC-1999 11-SEP-1999 11-SEP-2000 11-MAN-2000 11-MA

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9805-0088033P.
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15-MAR-2000;
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23-AUG-2000;
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                                                                     1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGCCTGTGTCCTGCAGCTCGTGCT
                                                                                                                               TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                      79 ATGAAGCTCGCCCCCCCCTCTGGGCTCTGCGTGGCCCTGTCTGCAGCTCCGCTGCTGCT
                                                                                                                                                                                             CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGGCT
                                                  Gaps
                                                 0;
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                             Length 570;
                                                 Indels
                            Score 308.8; DB 7;
Pred. No. 4.3e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane protein cDNA, #163.
                                                                                                                                                                                                                                                                                                                                                ABX90363 standard; cDNA; 570 BP
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9705-0062250P.
9705-0065186P.
9705-0065311P.
9705-0065311P.
9805-0078910P.
9805-0083322P.
9805-008760P.
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28-JUL-2000; 2000WO-US022710.
11-AUG-2000; 2000WO-US022031.
                           99.0%;
99.4%;
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                           Query Match
Best Local Similarity 99.4
Matches 310; Conservative
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28-MAY-1998;
02-JUN-1998;
02-JUN-1998;
02-JUN-1998;
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04-JUN-1998;
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12-NOV-1997;
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28-APR-1998;
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(GETH) GENENTECH INC.

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Claim 2; Fig 289; 650pp; English.
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                WPI; 2003-288106/28.
P-PSDB; ABU60604.
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Zhang Z;
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99.08; 99.48;

Human, PRO polypeptide; secreted protein, transmembrane protein, genetic disorder; antibacterial; immunosuppressive; transgenic; cDNA encoding human PR01245 polypeptide. 97WO-US020069. 97US-00651B6P. 97US-0066710P. 98US-0078910P. 98US-0078910P. 98US-0087607P. 98US-0087609P. 98US-0087759P. 98US-0087827P. 98US-0088021P. 98US-0088025P. 9803-0088033P. 9803-0088326P. 9803-0088167P. 9803-0088202P. 98US-0088824P 98US-008886EP 98US-008886EP 98US-0089105P 98US-0089105P 98US-0089512P 98US-0089512P 98US-0089538P 98US-0089538P 98US-0089538P 98US-0089538P 98US-0089538P 98US-0089538P 98US-0088212F 98US-0088655P 98US-0088734P 98US-0088738P 98US-0088742P 98US-0088028P. 98US-0088029P. 98US-0088030P. 98US-0084600P. 98US-0087106P. (first entry) gene therapy; gene; ss US2002103125-A1. Homo sapiens 20-NOV-2001; 05-NOV-1997; 12-NOV-1997; 13-NOV-1997; 24-NOV-1997; 25-FEB-1998; 20-MAR-1998; 28-APR-1998; 04-JUN-1998; 05-JUN-1998; 05-JUN-1998; 07-MAY-1998; 28-MAY-1998; 04-JUN-1998; 04-JUN-1998; 01-AUG-2002 10-JUN-1998 10-JUN-1998 1-JUN-1998 .7-JUN-1998 18-JUN-1998 The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or plantic acid activity of a cell. The PRO polypeptides or plantication, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in cissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABX90083-ABX90468 are the penalty of the primers amplifying and the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent sequence. Is also available in electronic format from USPTO at sequence.thml 0 139 TICITAGIGGCICGGCCAAGCCIGIGGCCCAGCCIGICGCIGCGCIGGAGICGGCGG 198 GAGGCCGGGGCCCGGACCCTGGCCAACCCCCTCGACCCGGTGAAGCTCCTG 180 258 318 GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGGAGGGGCCCTG Ρ. gene therapy, in chromosome identification, as 61 TICTIAGIGGGCICGGCCAAGCCIGTGGCCCAGCCIGICGCIGCGCGCGAGTCGGCGCCG GAGGCCGGGGCCGCGCACCCTCGCCACCCCTCGGCACCCTCAACCTCGTG CTGAGCAGCCTGGGCATCCCCGTGAACCACACATAGAGGGCTCCCAGAAAGTGTGTGGCT Godowski P Paoni NF; Wood WI; 1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCTGTGCTGCAGCTCCGCTCGTGCT CTGAGCAAGCCTGGGCCATCCCCCGTGAACCACCTCATAGAGGGCTCCCCAGAAGTGTGTGGCTT GAGCTGGGTCCCCAGGCCGTGGGGCCCTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG Gaps 0; New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identifica chromosome markers, or in generating probes. Length 570; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other; Indels Score 308.8; DB 7; Pred. No. 4.3e-53; 0; Mismatches 2;

99WO-US005028

08-MAR-1999;

ABX64209;

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking hioactive molecules to cells expressing PRO polypeptides, for inking biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The polymucleotide sequences chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of pRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the construct hybridisation malysis of malysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequata.uspto.gov/psipsDIDEntry.html
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P-PSDB; ABU13986.
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Godowski PJ; Paoni NF; Wood WI;

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                                                                                                                                                            GAGGCCGGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCCGCTGAAGCTCCTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted and transmembrane protein; cytostatic; anti-HIV; virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy; cancer; covarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
                                                                                                        61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG
                                                                                                                                                                                                              139 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
                                                                               1 ATGAAGCTCGCCCCCCCCCGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT
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Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
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Pred. No. 4.3e-53;
0; Mismatches 2;
                                                     0; Mismatches
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97US-0065186P.
97US-0065311P.
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                                                    Matches 310; Conservative
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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-973, 819-PTRA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Those care particularly useful for detecting or treating e.g. malignancies or lenkamia or lymphoma,), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases.

CC and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA.

The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's DL; Godowski PJ; Paoni NF; Wood WI; Arganderedecedecerecreseserereseseserererereresesereere TICTTAGTGGGCTCGGCCAAGCCTGTGGCCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG GAGGCCGGGGCCGGGACCCTGGCCAACCCCTTGGCCACCCTCAACCCGGTGAAGCTCCTG .. 0 Score 308.8; DB 7; Length 570; Pred. No. 4.3e-53; 0; Mismatches 2; Indels 0 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Perraraa N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other; Claim 1; Fig 289; 663pp; English. 0 29-JUN-2001; 2001WO-US021066. 09-JUL-2001; 2001WO-US021735. 28-AUG-2001; 2001US-00941992. 20-JUN-2001; 2001WO-US019692 tch 99.0%; al Similarity 99.4%; 310; Conservative ((GETH) GENENTECH INC. WPI; 2003-352829/33 P-PSDB; ABU72571. Local Similarity 19 121 61 139 Zhang Z; Query Match disease Matches g δ ò ПÞ à

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198 180 258 240 318 300

GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 378

ACAGIGITIGGC 312 ACAGIGITIGGC 390

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GAGGCCGCGCCCCCCTCCCCAACCCCCTCGCCACCTCAACCCCGCTGAAGCTCCTC CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT CTGAGCACCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCT GAGCTGGGTCCCCAGGCCGTGGAGGCCCTGAAGGCCCTGCTGGGGCCCTG

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Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy; tumour-associated antigenic target; TAT; ADBPT; antibody-dependent enzyme mediated prodrug therapy; cytostatic.
                                                                        Human secreted/transmembrane protein cDNA, #163.
                  ABX80890 standard; cDNA; 570 BP.
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9805-0084600P

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RESULT 15
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PR 19-UN-1998 980S-0089347P
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PR 22-UN-1998 980S-0090244P
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PR 10-UU-1998 980S-009163P
PR 10-UU-1998
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PR 26-AUG-1998; 99US-0097954P.
PR 26-AUG-1998; 99US-0097954P.
PR 26-AUG-1998; 99US-0097974P.
PR 26-AUG-1998; 99US-0097974P.
PR 26-AUG-1998; 99US-0097974P.
PR 26-AUG-1998; 99US-0097974P.
PR 26-AUG-1998; 99US-0099734P.
PR 31-AUG-1998; 99US-0099852P.
PR 31-AUG-1998; 99US-0100834P.
PR 31-AUG-1998; 99US-0100834P.
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PR 17-SEP-1998; 99US-0100834P.
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PR 07-CT1999; 99US-0113296P.
PR 02-JUN-1999; 99US-0123957P.
PR 02-JUN-1999; 99US-01396P.
PR 26-JUN-1999; 99US-0146222P.
PR 26-JUN-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0146228P.
PR 18-SEP-1999; 99US-014622P.
PR 19-AUR-1999; 99US-0146228P.
PR 19-AUR-2000; 2000WG-US00131P.
PR 19-EEB-2000; 2000WG-US00131P.
PR 19-EEB-2000; 2000WG-US00131P.
PR 19-AUR-2000; 2000WG-US00131P.
PR 21-AUR-2000; 2000WG-US0023328.
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ö GAGGCGGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCGGCTGAAGCTCCTG 180 138 120 09 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCTGTCGCTGCGCTGGAGTCGGCGGCG Gaps . 0 Length 570; Indels Score 308.8; DB 7; Pred. No. 4.3e-53; 0; Mismatches 2; : 0 Query Match
Best Local Similarity 99.4%;
Matches 310; Conservative (139 79 19 121

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 QY
 181 CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGCTCCCAGAAGTGTCTGGCT
 240

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 259 CTGAGCAGCCTGGGGCATCCCCGTGAACGCTCCCAGAAGTGTGTGGCT
 318

 QY
 241 GAGCTGGGTCCCCAGGCCGTGAAGGCCCTGAAGGCCTTGCTGGGGGCCCTG
 300

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 319 GAGCTGGGTCCCCAGGCGCTGAAGGCCCTGAAGGCCTTGCTGGGGGCCCTG
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 301 ACAGTGTTTGGC
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 390

6, 2004, 14:21:42

Search completed: June Job time : 344 secs

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nucleic	eic search, using sw model
Run on:	June 6, 2004, 13:39:06; Search time 2499 Seconds (without alignments) 3728.291 Million cell updates/sec
Title: US Perfect score: 31 Sequence: 1	US-10-081-817A-3 312 1 atgaagctcgccctcctgggccctgacagtgtttggc 312
Scoring table: ID Ga	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 27	27513289 segs, 14931090276 residues
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Description	BM920793 AGENCOURT BM920794 AGENCOURT BM977626 UI-CP-EN1 BI818715 603037535
SUMMARIES	BM920794 BM977626 BI818715
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* Query Match Length DB ID	473 12 473 12 490 12 496 12
% Query Match	0.000.0000.0000000000000000000000000000
Score	308.8 308.8 308.8
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6030550 AGENCOU AGENCOU EST3868 NISC 9j UI-CF-E tt90f09.	B1490604 603032283 B1819014 603031310 B1819795 603041303 B1822360 603037920 B14887765 603032283 B1821791 603032883	qp98f05.x qe26d06.x 60303924- 60303305.wc34e01	wc36c10 7062e0 603032 w063a10 UI-CF- UI-CF- UI-CF-	59 60303 98 60307 1 wa84h0 7 nx30g0 zd61a04 98 NISC	4 zallbuz 64 ns54a0 788 60303 00 ok69a0 758 QV3-H 439 UI-CF 2 zb52d10
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ALIGNMENTS

BM920793 AGENCOURT_6705937 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752038 5', mRNA sequence. BM920793 BM920793.1 GI:19371172 EST. Homo sapiens (human)	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 473) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Email: Gapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov High quality sequence stop: 474.
BM9207 AGENCC 5', mb BM9207 BM9207 BM9207 HOMO E	Bukar Mamma. 1 (b) NIH-M NATION Unpubl Contac Email: Tissue CDNA CDNA CDNA CDNA CDNA CDNA CDNA CDNA
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Normalization and subtraction: two approaches to facilitate gene
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McCray Lab
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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DEFINITION

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ORGANISM

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BI818715.1 GI:15930265
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158 ACAGTGTTTGGC 147
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//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone_lib="UUI-CP-ENI"
//note="Organ: Lung, Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(8): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (IT)19 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Amman Lung Epithelial Cell Lines untreated LPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                        Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDN Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
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/db xref="taxon:9606"
/clone="UI-CF-EMI-aef-c-13-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
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                                                                                                                                                                                                                                                                                                                                                        Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA sequence: 459-484, AGC rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.
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                          2024 University of Iowa Med Labs, Iowa City, IA 52242, Tel: 319 356 4866 7171
Eax: 319 356 7.171
Email: paul-mccray@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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TAG LIB∺UI-CF-EN1
TAG SEQ=CTGCTCAGGT"
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/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/db_xref="laxon:9606"

/dlone="limAdS::515608"

/dlone="lim
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 496)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapDs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMILH45 row: e column: 09
High quality sequence stop: 471.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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021. Note: this is a NIH MGC Library
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99.4%; Pred. No. 2.5e-42;
iive 0; Mismatches 2;
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Contact: Robert Strausberg, Ph.D.
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/lab host="MHINDS"
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6759083 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5755192
    GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGCTGGGGGCCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Produzement: Life Technologies, Inc.
Tissue Produzement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov.m column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3e-42;
0; Mismatches 2;
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5755192"
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Best Local Similarity 99.4%;
Matches 310; Conservative
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5', mRNA sequence.
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
site_1: Not1; Site_2: BcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
                                                                                                                                                                                                                                                                                                                      BI769722 1004 bp mRNA linear BST 25-SEP-2001 603055021F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204452 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.go.row: j column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 GAGGCCGGGGCCGGGAACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 3
High quality sequence stop: 416.
Location/Qualifiers
1..1004
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/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI769722.1 GI:15761287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                       324 ACAGTGTTTGGC 335
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301 ACAGIGITIGGC
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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AW974727 550 bp mRNA linear EST 02-JUN-2000 EST386817 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
220
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                                                                                                               CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGCT 280
                                                                                                                                                                                                     241 GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTG 300
                                                                                                                                                                                                                                             GAGCTGGGTCCCCAGGCCGTGGGGGCCCTGAAGGCCCTGCTGGGGGCCCTG 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 550)
Hegde, P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9
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RESULT

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/dev stage="Adult"

/lab host="DH10B (Life Technologies) (TI phage resistant)"

/clone_11b="UI-CF-ENI"

/note="Organ: Lung, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-ENI is a normalized CDNA library containing the following tissue (8): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not oly and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dY)1B tail. The sequence tag for this library is CTGCTCAGGT.

TAG_INSUE-Human Lung Epithelial Cell Lines untreated LPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of lowa
University of lowa
2024 University of lowa Med Labs, lowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of lowa
CDNA Library preparation: Dr. M. Bento Soares, University of lowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                   EST 21-FEB-2003
                                                                                                                       GGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTGACAGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 472)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
     GGGTCCCCAGGCCGTGGGGCCCGTGAAGGCCCTGCTGGGGGGCCCTGCTGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
                                                                                                                                                                                                                                                                                                                                                                             BM977779
UI-CF-EN1-aef-n-17-0-UI.S1 UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UI-CF-EN1-aef-n-17-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
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/db_xref="taxon:9606"
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BM977779/c
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KEYWORDS
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/lab_host="adult"
/lab_host="btloB"
/clone_lib="NCI CGAp_Pr28"
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a medified polylinker; Plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapDS-r@mail.nih.gov

cDNA Library Preparation:

cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NOI-CGAP clone distribution information can be
                                                                                                                                                                                                      VISC_gj12e05.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271401 CB049699
265 GAGCIGGGICCCCAGGCCGIGGGGGCCGIGAAGGCCCTGAAGGCCCTGCTGGGGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cedeccededacceredecaacceceredecaecereaaccecereaage 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 437)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM8008 row: J column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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tt90f09.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248841 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cent
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="nH108"
/clone lib="NL1 GARP_Pr28"
/note="Grgan: prostate; Vector: pT7T3D-Pac (Pharmacia)
                                                                                                                                                                                                                                                                                                                                                      GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGTTGAAGCTCCTG
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                                                                                           12;
                                                                                             Score 299.8; DB 12;
Pred. No. 7.9e-41;
0; Mismatches 7;
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Seq primer: -40UP from Gibco.
Location/Qualifiers
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG SEQ=CTGCTCAGGT"
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Best Local Similarity 97.7%;
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with a modified polylinker, Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool 65,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo.
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603033186F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174540 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 961)

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k column: 21
Plate: LLAM11434 row: k column: 21
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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High quality sequence stop: 511.
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/db_xref="taxon:9606"
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/Glome_Tibe_Will MGC 115."
/folow="Organ: pooled brain, lung, testis; Vector:
pCWV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymus pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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603034390F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175502 5',
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.c column: 23
High quality sequence start: 4
High quality sequence stop: 405.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                             Score 297.8; DB 12; Length 961;
Pred. No. 2.1e-40;
); Mismatches 2; Indels 1;
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Matches 310; Conservative
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/lab host="DRIOR"
/done lib="NIH MGC 115"

source anonymous pool of 6 male brains, age range 23-27; la male ling, age 27; and 1 male testis, age 60. Library is oligo-dT primed and directionally cloned (Bookv site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021, Note: this is a NIH_MGC Library."
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603032283T1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5173268 3',
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I (bases 1 to 416)

NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Pred. No. 2.4e-40;
0; Mismatches 2; Indels 1;
                                                 'clone="IMAGE:5175502"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone lib="NHIH MGC 115"
/clone lib="NHH MGC 115"
/clone lib="NHH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male_brains, age range 23-27;
nale lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Issue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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99.0%; Pred. No. z...
... 0; Mismatches
                                                                                                                                                                                                             organism="Homo sapiens"
High quality sequence start: 6
High quality sequence stop: 416.
Location/Qualifiers
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'db_xref="taxon:9606"
'clone="IMAGE:5173268"
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BI819014.1 GI:15930564
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**Note=_Cragan: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; nale of prime and the properties, age 59. Library is onlige-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLAMI1434 row: k column: 07
High quality sequence stop: 470.
Location/Qualifiers
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                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                           /lab_host="DH108"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                      'clone="IMAGE:5174526"
                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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USA
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Sequence 3615, Ap
Sequence 13281, A
Sequence 12677, A
Sequence 13122, A
Sequence 7316, Ap
Sequence 7116, Ap
Sequence 7116, Ap
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Sequence 4, Appli
Sequence 5, Appli
Sequence 267, App
Sequence 47, Appl
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11, Appl
7385, Ap
48, Appl
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Sequence 37, Appl
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2164.308 Million cell updates/sec
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Sequence 50,
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/egn2_6/ptodata/2/ina/5B_COMB.seq:*
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/egn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-964-725-4

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US-09-252-991A-3615

US-09-252-991A-3615

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US-09-252-991A-12820

US-09-252-991A-13281

US-09-252-991A-13820

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Maximum Match 100%
Listing first 45 summaries
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88 84 44 8 8 9 0 11	4 4 4 4 0 0 0 0	133.55 133.55 135.55	13842 36778 38506 38506	w w w 4	US-09-105-537-30 US-09-105-537-5 US-09-320-878-19 US-09-141-908-1	Sequence 3 Sequence 5 Sequence 1 Sequence 1	0,0,
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ALIGNMENTS

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US-08-964-725-5
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STRANDEDNESS:
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93;
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US-08-964-725-5
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                             Score 56.4; DB 2; Length 263; Pred. No. 0.0013; 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       FREEDMAN, Paula N.
GORDON, Julian
HODGES, Steven C.
KLASS, Michael R.
KRATOCKUTL, Jon D.
ROBERTS-RAPP, Lisa
RUSSELL, John C.
STROUDE, Steven D.
INVENTION: REACENTS AND METHODS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56.4; DB 2;
Pred. No. 0.0014;
                                                                                                                                                                                                                             257 CCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCT 290
                                                                                                                                                                                                                                                              180 CTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 213
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 5997.US.Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08964725
Patent No. 5939265
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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60.4%;
                                  18.1%;
60.4%;
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                                                                                                                                                                                                                                                                                                                                                                                              COHEN, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                Query Match 18.1
Best Local Similarity 60.4
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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linear
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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Best Local Similarity
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US-08-964-725-4
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Indels
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TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56.4; DB 2;
Pred. No. 0.0014;
0; Mismatches 61;
                                                                                                                                                                                                                      CCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCT 290
                                                                                                                                                                                                                                                             315 crrcrcaaccrcrcaacaacrccrccaccccr 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastERQ for Windows Version 2.0 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
  Mismatches
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100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08964725 Patent No. 5939265
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COHEN, Maurice
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLASS, Michael R.
APPLICANT: RASTOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: RUSSELL, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 REFERENCE/DOCKET NUMBER: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.1%;
Best Local Similarity 60.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIAL
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 519 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
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1339 CAAGCTAACCACGCTGGTGGATGCCGACGCCGAGGCCTTCACCGCCTACCTGGAAGCAAT 1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1279 ATTCCAGTCCCTGGACACGACGATGCGGCCTGATCCCGCCCTTCCGCGAGGCTTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGCCTGCTGCAGCTCCGCGCTCGTTTT
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TITLE OF INVENTION: No. 66696621 Nucleic Acids and
TITLE OF INVENTION: No. 666966221 Nucleic Acids and
TITLE OF INVENTION: POLYPEPTIGE
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PLING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL FL genes Version 1.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 148;
321 TGAAGCTGTGAAGAAACTGCTGGAGGCGCT 350
                                                                                                                                                                                               Sequence 47, Application US/09620312D Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(2497)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-47
                                                                                                                                                                                                                                                                                 Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Felyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     John Tillinghast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou, Ping
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (107)..(1756)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang,
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NAME/KEY: CDS
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                                         원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GACAAACATTCTTCCCTTTATGGATCCATTAAAGCTTCTTCTGAAAACTCTGGGGCATTTC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOTTGAGCACCTIGIGAGGGGCTAAGGAAGTGTTAAATGAGCTGGGACCAGAGGCTTC 320
   208 CTCTGGACAACATTCTTCCCTTTATGGATCCATTAAAGCTTCTTCTGAAAACTCTGGGCA 267
                                                                 197 TCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGG 256
                                                                                                                              268 TITCIGITGAGCACCITGIGGAGGGCTAAAGGAAGTGIGIAAATGAGCTGGGACCAGAGG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Scilamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: SERRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
bT1.ING DATE: HEREWITH
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                                                                                                                                                                                            257 CCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCT 290
                                                                                                                                                                                                                                                             328 circigaagcigigaaagaaacigcigaaggggcii 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA-0001
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 267, Application US/09023655 Patent No. 6607879
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHAR
STREET: 3174 PORTER DR
CITY: PALO ALTO
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LIBRARY: LUNGNOT01
; CLONE: 126758
US-09-023-655-267
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               US-09-023-655-267
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GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITILE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubenfield et al. NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GGGCTCGGCCAAGCCTGTGGCCCAGCCTGTGCGCTGGAGTCGGCGGCGGCGGCGG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                281 Grecheancecerricaececesaacaecescescescescescescescesces 340
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Pred. No. 0.18;
0; Mismatches 158;
   Mismatches 104;
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CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION:
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Best Local Similarity 47.2%;
Matches 141; Conservative
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US-09-252-991A-13281/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                 Sequence 3660, Application US/09252991A Patent No. 6551795
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Best Local Similarity 51.2%;
Matches 109; Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 3615
LENGTH: 3297
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APPLICANT: Marc J.
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LENGTH: 2274
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PELLORION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13122, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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Patent No. 6551795
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Best Local Similarity
Matches 141; Conserv
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US-09-252-991A-13122/c
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US-09-252-991A-7316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                894 GATCGCCAACGACCTGCGCCTGCTCGGTTCCGGCCCACGCGCCCGGCTTCGCCGAGGTGAA 953
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AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 0.18;
0; Mismatches 158; Indels
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Pred. No. 0.18;
0; Mismatches 158;
                            FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
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Sequence 12677, Application US/09252991A
Patent No. 6551795
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47.2%;
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larity 47.2%;
Conservative
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SEQ ID NO 12677
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Matches 141; Conserv
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Best Local Similarity
Matches 141; Conserv
TITLE OF INVENTION:
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APPLICANT: Marc J.
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LENGTH: 1425
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                   206 ACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGG 265
                                                                                        169 ACCAGAGGGTCGACGACGCGTTGCAGACCGAGGCGGCGCTGGGCAACATCGCCACGGCGG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 GGGCGCTGGCGCGCGCGCACCCCAACAGTCCACGGCCGAGATCGAGACCCTGATCGGTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 TCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCTTTCTTAGTGGGCTCGGCCAAGCCTG
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APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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Pred. No. 0.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-252-991A-7304/C
; Sequence 7304, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08555669
Patent No. 5773248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCGCTGATCCAGCAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 CCGTGAAGGCCCTGAAG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.0%;
Matches 131; Conservative
                                                                                                                                                                 266 CCGTGAAGGCCCTGAAG
                                                                                                                                                                                                                                       109 redcecréarceacae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: N
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.

TITLE OF INVENTION: AERCHOINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196 136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCGGGCCGGGGCCGGGACCCTGGCCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 ACCAGAGGGTCGACGACGCGTTGCAGACCGAGGGGGGCCTGGGCAACATCGCCACGCGG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 TGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCGGGGCCGGGGCCGGGACCCTGGCCA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 GGGCGCTGGCGCGCCGCCCAACAGTCCACGGCCGAGATCGAGACCTGATCGGTGCCT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 TCGAGGCGCGCGCGCCGCCGCGACCAGGGTCGAGGCTTCGCCGTGGTCGCCGACGACGAGGTGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 ACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 Tecagaandecacedecacadecederecaecatandeaecedeaecaccaente---eneg 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCGTGGCCCTGTCCTGCTCGCTCGTGCTTTTTAGTGGGCTCGGCCAAGCCTG 85
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.2%; Score 44.2; DB 4; Best Local Similarity 51.0%; Pred. No. 0.46; Matches 131; Conservative 0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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Pred. No. 0.
                                              60/094,190
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                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 CCGTGAAGGCCCTGAAG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 TGGCGCTGATCCAGCAG 493
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.0%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                            US-09-252-991A-7316
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                                                                                                                                                      SEQ ID NO 7316
LENGTH: 729
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                                                                                                                                                                                                                               TYPE: DNA
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1211 GOCCTOGGOCCACAAGGOCCTTCCCGAAGCCCTGGTGTCCGAGGCTTCCAGGGCCAGAAG 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTGCGCTGGAGTCGGCGGCGGAGGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTGAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 CAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%; Score 44.2; DB 1; Length 2543; 47.3%; Pred. No. 0.49; tive 0; Mismatches 148; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1451 GCAGTCGAGGGAGCTGGGCCCCAAAGGCACCCAGGGTCC 1491
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBRA: US/08/555,669
FILING DATE: 1-NOV-1995
CLASSIFICATION: 435
ATTONREY/AGBNT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/POCKET NUMBER: 8389-030
TELEPRA: 415-854-366
TELEPRA: 415-854-366
TELEPRA: 415-854-369
TELEPRA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.35
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
) LOCATION: 47..2098
US-08-555-669-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
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Search completed: June 6, 2004, 15:43:07 Job time: 81 secs Sequence 407, App Sequence 407, App

US-09-991-163-407
US-09-993-664-407
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Sequence 407,
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result
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-211-85-6

US-10-211-864-27

US-09-989-723-407

US-09-989-723-407

US-09-989-723-407

US-09-989-73-407

US-09-989-73-407

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US-09-991-73-407
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                                                                                                                                                                                                                                                               2995936 seqs, 2280998010 residues
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                                                         nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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ALIGNMENTS

RESULT

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seg:∗	US-10-081-817-3
.sed:*	; Sequence 3, Application US/10081817
3.seq:*	; Publication No. US2002018350121
3.seg:*	GENERAL INFORMATION:
.seq:*	; APPLICANT: Polvak. Kornelia
.seq2:*	; APPLICANT: Porter, Dale
3.seg:*	
3.seg:*	; APPLICANT: Krop, Ian
3.seg:*	
.sed:*	FILE REFERENCE: 00530-094001
.seg:*	CURRENT APPLICATION NUMBER: US/10/081.817
sed:*	; CURRENT FILING DATE: 2002-05-31
•	; PRIOR APPLICATION NUMBER: 60/270,973
e to have a	; PRIOR FILING DATE: 2001-02-23
t being printed,	PRIOR APPLICATION NUMBER: 60/351,908
ution.	; PRIOR FILING DATE: 2002-01-25
	; NUMBER OF SEO ID NOS: 32
	; SOFTWARE: FastSEO for Windows Version 4.0
	; SEQ ID NO 3
	; LENGTH: 312
Description	; TYPE: DNA
	ORGANISM: Homo capiene
Sequence 3, Appli	US-10-081-817-
Sequence 18, Appl	
Sequence 6, Appli	Query Match 100.0%; Score 312; DB 14; Length 312.
27,	Similarity 100.0%; Pred, No. 8.2e-68;
27,	vative 0
Sequence 407, App	2y 1 ATGAAGCTCGCCCCTCTGGGGCTCTGCCTGCCTGCAGCTCCAGCTCGCTGCAGCTCAGCTGCAGCTCGCTGCAGCTCGCTGCAGCTCGCTGCAGCTCGCTGCAGCTTGCAGCTCAGCTAGCT
Sequence 407, App	
	Db 1. ATGAAGCTCGCCCTCCTGGGGCTCTGCGTGGCCCTGTGCAGCTCTGTAGTTCTTGCTTCTTGTAGTTGTTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
407,	
	Qy 61 TICTIAGIGGCTCGGCCAGCCTGTGGCCTGTGCTGCTGCTGCAGCTGAAGCCTGTGAAGAG
Sequence 407, App	Db 61 TTCTTAGTGGGCTCGGCCTGTGGCCCAGCCTGTCGCTGCGCTGCAGTCGGCGGCG
Segmence 407. App	

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GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTTGGCACCCGTCAACCCGCTGAAGCTCCTG 180

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61 ITCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 120
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; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6
                                Sequence 6, Application US/10237435
Publication No. US20030124580A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wichael G.
APPLICANT: Wichael G.
APPLICANT: Mirry, Lynn B.
TITLE OF INVENTION: LUNG SURFACTANT MOLECULES
FILLE REFERENCE: PH-0019 US
CURRENT APPLICATION NUMBER: US/10/237,435
CURRENT FILING DATE: 2002-09-06
FRIOR FILING DATE: 09-07-2001
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/10211858; Publication No. US20030211096A1; GENERAL INFORMATION:
APPLICANT: Goddard, Audrey; APPLICANT: Goddard, Audrey; APPLICANT: Godowski, Paul J.; APPLICANT: Hillan, Kenneth J.; APPLICANT: Hillan, Kenneth J.; APPLICANT: Pattik, Rabattant APPLICANT: Pitti, Robert M.; APPLICANT: Pitti, Robert M.; APPLICANT: Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.08;
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Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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Best Local Similarity 99.4'
Matches 310; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
TRNGTH: 561
RESULT 3
US-10-237-435-6
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CURRENT APPLICATION NUMBER: US/10/426,002
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
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                                                                                                                                                            GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCGCGCTGAAGCTCCTG 267
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  121 GAGGCCGGGGCCGGGACCCTAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 180
                                                                                                                                   1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCTGTCCTGCAGCTCCGCTCGTGCT 60
                                                                         181 CTGAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGGGCT
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                                                CTGAGCAGCCTGGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGGT
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10426002
Publication No. US20040101876A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azar, Idit
Bernstein, Jeanne
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Freilich, Shiri
Beck, Nili
Zhu, Wel-Yong
Wasserman, Alon
Hermesh, Chen
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Best Local Similarity 99.4
Matches 310; Conservative
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APPLICANT: Xie, Hanging
APPLICANT: Dahari, Dvir
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US-10-426-002-18
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APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILLE NETERERCE: P2931RIC1
CURRENT APPLICATION NUMBER: US/10/211,858
CURRENT FILING DATE: 1996-09-23
PRIOR PELING DATE: 1996-09-33
PRIOR PELING DATE: 1996-09-33
PRIOR PELING DATE: 1996-09-23
PRIOR PELING DATE: 1996-09-3
PRIOR PELING DATE: 1997-09-19
PRIOR PELING DATE: 1997-10-10
PRIOR PELING DATE: 1997-10-10
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-11-24
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PRIOR PRI
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Pred. No. 4.6e-67;
0; Mismatches 2;
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Publication No. US0030170228A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
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Matches 310; Conservative
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ORGANISM: Homo sapiens
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US-10-210-951-27
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Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Hillan, Kenneth J. Marsters, Scot A.

APPLICANT: APPLICANT: APPLICANT:

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                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P2931R1C1
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Pred. No. 4.6e-67;
0; Mismatches 2;
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CURRENT PEPLICATION NUMBER: US/10/210,951
CURRENT FILING DATE: 2002-08-02
PRIOR PAPPLICATION NUMBER: 06/014699
PRIOR PILING DATE: 1996-04-01
PRIOR PILING DATE: 1996-04-01
PRIOR PAPLICATION NUMBER: 60/059121
PRIOR APPLICATION NUMBER: 60/059121
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR FILING DATE: 1997-07-17
PRIOR FILING DATE: 1997-01-01
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-24
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; Sequence 27, Application US/10211884
; Publication No. US20030175900A1
; GENERAL INFORMATION:
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99.4%;
                                                                                                                      Watanabe, Colin K. Wood, William I.
Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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                                                                                               Stone, Donna M.
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US-10-210-951-27
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Best Local Similarity
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ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
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NUMBER OF SEQ ID NOS: 258
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Pred. No. 4.6e-67;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-10-24
PRIOR PELLING NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION WUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
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Smith, Victoria
                                                                                  Hillan, Kenneth J
                                         Godowski, Paul J. Gurney, Austin L.
                                                                                                   Marsters, Scot A
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Ashkenazi, Avi J.
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Best Local Similarity 99.4
Matches 310; Conservative
                                                                                                                                                                                                      Stone, Donna M.
                                                                                                                                                                                                                                                                                        FILE REFERENCE: P2931R1C1
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LENGTH: 569
TYPE: DNA
ORGANISM: Homo sapiens
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IIILE OF INVENTION: Acids Encoding the Same
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PRIOR PLING DATE: 1997-06-16
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PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1999-02-25
PRIOR PILING DATE: 1999-02-25
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PRIOR PILING DATE: 1999-02-25
PRIOR PILING DATE: 1999-02-05
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1998-03-07
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-04
; Sequence 407, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Gerritsen, Mary E.
Goddard, Audrey
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                                                                                       APPLICANT: Ashkenazi, Avi J
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Botstein, David
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Eaton, Dan L.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Watanbe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wold, William I.
APPLICANT: Wold, Sceneted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILIS REFERENCE: 1973-06-16
FILIS REFERENCE: 1970-06-16
FRICK APPLICATION NUMBER: 60/049787
FRICK FILING DATE: 1997-10-17
FRICK APPLICATION NUMBER: 60/065311
FRICK FILING DATE: 1997-11-12
FRICK APPLICATION NUMBER: 60/065311
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FRICK APPLICATION NUMBER: 60/065311
FRICK FILING DATE: 1997-11-24
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FRICK FILING DATE: 1998-04-28
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                                                                                                319 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 378
                                         CTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGTGGCT
                                                                                                                                                                                                                                             Sequence 407, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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PRIOR FILLING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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Gurney,Austin L
Kljavin,Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
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Eaton, Dan L.
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-16
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APPLICATION NIMBER: 60/088810
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089105
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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NUMBER: 6(1) 1998-03-7(1) 1998-03-7(1) 1998-05-7(1) 1998-05-7(1) 1998-05-7(1) 1998-06-1 1998-06-	NUMBER: 60, NUMBER	1998-06- NUMBER: 6 1998-06- NUMBER: 6 1998-06- NUMBER: 6 1998-06- NUMBER: 6 11998-06-
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PRIOR PLILING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PLILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 GAGGCCGGGGCCGGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG 258
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730PLG65
CURRENT APPLICATION NUMBER: US/09/989,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 308.8; DB 9
Pred. No. 4.6e-67;
0; Mismatches 2
                                  PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FLING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PLING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-09
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Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
APPLICATION NUMBER: 60/091626
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.0%;
Best Local Similarity 99.4%;
Matches 310; Conservative
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Goddard, Audrey
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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PRIOR FILING DATE: 1997-66-16

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PRIOR PAPLICATION NUMBER: 60/06518

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-11-12

PRIOR PLING DATE: 1997-10-13

PRIOR PLING DATE: 1997-10-13

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PRIOR PRIOR DATE: 1996-06-03

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PRIOR PRIOR DATE: 1996-06-07

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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
                                                                              APPLICATION DATE: 1998-U6-10
APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090535
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
                  FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER:
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121 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCTGAAGCTCCTG 180 241 GAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300 TICTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGCGCG 120 79 Argaagcreececerecresses reneral de la consecue del la consecue de la consecue 199 GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG creaecaeccreeecarceccereaaccaccrearaeaeecreecaeaagrererer ATGAAGCTCGCCCCTCCTGGGGCCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT Gaps 0 570; Length Indels Score 308.8; DB 9; Pred. No. 4.6e-67; 0; Mismatches 2; R APPLICATION NUMBER: 60/090862

RR APPLICATION NUMBER: 60/090862

RR FILING DATE: 1998-06-26

RR FILING DATE: 1998-06-26

R FILING DATE: 1998-06-26

R FILING DATE: 1998-06-26

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/09154

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/09154

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/09159

R APPLICATION NUMBER: 60/091625

R APPLICATION NUMBER: 60/09163

R FILING DATE: 1998-07-07

R APPLICATION NUMBER: 60/09182 Sequence 407, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION: Grimaldi,J.Christopher Gurney,Austin L. Kljavin,Ivar J. Napier,Mary A. 99.0%; Eaton, Dan L. Ferrara, Napoleone FILING DATE: 1998-07-09 Gerritsen, Mary E Gerber, Hanspeter ACAGTGTTTGGC 312 Query Match
Best Local Similarity 99.0
Matches 310; Conservative 379 ACAGTGTTTGGC 390 APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc Goddard, Audrey Godowski, Paul Fong, Sherman US-09-989-731-407 61 139 181 259 301 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: RESULT 11 PRIOR
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PRIOR APPLICATION NUMBER: 60/08824
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PRIOR PELING DATE: 1988-06-10
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PRIOR PILING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-11
PRIOR PELING DATE: 1998-06-11
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PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/08876
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-16
PRIOR PILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
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PRIOR PILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/08948

PRIOR PELING DATE: 1998-06-19

PRIOR PELING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/08952

PRIOR PELING DATE: 1998-06-2

PRIOR APPLICATION NUMBER: 60/090254

PRIOR PELING DATE: 1998-06-2

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                      APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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FILING DAFE: 1998-06-24
APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090472
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
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CURRENT FILING DATE: US/09/989,731
CURRENT APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/088028
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088202
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087759
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FILING DATE: 1998-06-04
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                                                                                                                            Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                        Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J. Grimaldi, J. Christopher

Goddard, Audrey

Gurney, Austin L. Kljavin, Ivar J.

Napier, Mary A.

APPLICANT

Ferrara, Napoleone Gerber, Hanspeter Gerritsen, Mary E.

Eaton, Dan L.

Fong, Sherman

NUMBER: 60/090557

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1larity 99.4%; Pred. No. 4.6e-67;
Conservative 0; Mismatches 2.
PRIOR FILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
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PRIOR PRILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091633
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Best Local Similarity
Matches 310; Conserv
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Sequence 407, Application US/09989732 Patent No. US20020123463A1 GENERAL INFORMATION: APPLICANT: Ashkenai, Avi J. APPLICANT: Baker, Kevin P.

US-09-989-732-407

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and Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                     TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC57
                                                                                                                                                                                                                                                                                                                FILE KEFEKENCE: 27.09LC3.

CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PELLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-01-17
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1998-02-25
PRIOR PELLING DATE: 1998-02-07
PRIOR PELLING DATE: 1998-05-29
PRIOR PELLING DATE: 1998-06-02
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
                                                     Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                               Roy, Margaret Ann
Stewart, Timothy A.
Paoni, Nicholas F.
                                                                                                                                                                                                            Zhang, Zemin
APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR PLICATION NUMBER: 60/088212
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PRIOR PRILING DATE: 1998-06-05
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IOR	PPLICATION NUMBER: 60
TRICK	FILLING DATE: 1998-06-24
PRIOR	ILING DATE: 1998-06-24
PRIOR	PPLICATION NUMBER: 60
PRIOR	FILING DATE: 1998-06-24
PRIOR	ILING DATE: 1998-06-24
PRIOR	ATION NUMBER: 6
PRIOR	: 1998-06-24
2 6	APPLICATION NUMBER: 60/090542
PRIOR	APPLICATION NUMBER: 60/090557
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RIOR	APPLICATION NUMBER: 60/090694
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PRIOR	APPLICATION NUMBER: 60/090695
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PRIOR	APPLICATION NUMBER: 60/090862
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PRIOR	ATION NUMBER: 6
RIOR	1998-07-01
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RIOR	1998-07-01
PRIOR	NUMBER: 60
RIOR	1998-07-02
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PRIOR	NUMBER: 60
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	139 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG 1.
	121 GAGGCCGGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCTGAAGCTCCTG
	199 GARGEOGRAGA CHUMARANDA AND CONTROLES CARGARA CONTROLA CARGARA CONTROLA
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	181 CTGAGCCTGGGCATCCCCGTGAACCACTCATAGAGGGCTCCCAGAAGTGTGTGGCT
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730P1CL3 CURRENT APPLICATION NUMBER: US/09/991,073 CURRENT FILING DATE: 2001-11-14 PRIOR PAPLICATION NUMBER: 60/062250 PRIOR PILING DATE: 1997-06-16 PRIOR PILING DATE: 1997-06-16 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-11-12 PRIOR PILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-13 PRIOR FILING DATE: 1997-11-14 PRIOR FILING DATE: 1997-11-15 PRIOR FILING DATE: 1997-11-15 PRIOR FILING DATE: 1997-11-25 PRIOR FILING DATE: 1998-0.2.55 PRIOR FILING DATE: 1998-0.2.25
                                                                                                                                                                                                                                                                     Sequence 407, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/07910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/087607
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Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
301 ACAGIGITIGGC 312
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Napier,Mary A.
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Godowski, Paul
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Eaton, Dan L.
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
APPLICATION 1998-06-19
APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/088376 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/089907 FILING DATE: 1998~06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089948 ION NUMBER: 60/088028 ATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/08861 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088029 1998-06-18 FILING DATE: 1998-06-22 1998-06-19 FILING DATE: 1998-06-04 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 FILING DATE: 1998-06-17 FILING DATE: 1998-06-10 1998-06-12 FILING DATE: 1998-06-1 FILING DATE: ILING DATE: FILING DATE: FILING DATE: PRIOR
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/090252

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RESULT 14
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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Best Local Similarity 99.4%;
Matches 310; Conservative
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AFPLICANT: Zhang, Zemin I.

PEPLICANT: Zhang, Zemin I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/990,442

CURRENT APPLICATION NUMBER: 60/06250

PRIOR PILING DATE: 1997-06-16

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-12

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1997-11-24

PRIOR PILING DATE: 1998-02-25

PRIOR PILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-26

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-05-26

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GAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG
                                               GAGGCCGGGGCCGGGACCCTGGCCTCGGCACCCTCAACCCTGAAGCTCTG
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Patent No. US20020132252A1
PERERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
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R FILING DATE: 1998-06-24
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RETLING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 FILING DATE: 1998-07-02 FILING DATE: 1998-06-25 FILING DATE: 1998-06-18 PRIOR
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C17
                                                                                                                                                                                                                                                                                                                            1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGGCTCGTGCT
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                0;
                                                                                                                              Score 308.8; DB 9; Length 570; Pred. No. 4.6e-67; 0; Mismatches 2; Indels 0
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CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/05186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/05311
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Patent No. US20020132253A1
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Grimaldi,J.Christopher
Gurney,Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
                                                                                                                                   99.0%;
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Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 ACAGIGITITGGC 390
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APPLICANT: Ashkenazi, Avi J.
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                                                                                                                                                                               Best Local Similarity 99.4
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker, Kevin P.
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APPLICANT:
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                                                                                                                                        Query Match
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
                                                                APPLICATION NUMBER: 60/075945
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FILING DATE: 1998-03-20
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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1997-11-13
                                                                                          FILING DATE: 1998-02-25
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PRICR PELICATION NUMBER: 60/08532

PRICR FILING DATE: 1938-06-17

PRICR APPLICATION NUMBER: 60/08538

PRICR APPLICATION NUMBER: 60/08599

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PRICR APPLICATION NUMBER: 60/08509

PRICR APPLICATION NUMBER: 60/08501

PRICR PILING DATE: 1938-06-17

PRICR PILING DATE: 1938-06-18

PRICR PILING DATE: 1938-06-19

PRICR PILING DATE: 1938-06-19

PRICR PAPELICATION NUMBER: 60/08908

PRICR APPLICATION NUMBER: 60/08908

PRICR PILING DATE: 1938-06-29

PRICR PI
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Search completed: June 6, 2004, 16:47:38 Job time: 328 secs

138 120 240 198 180 258 318 GAGCTGGGTCCCCAGGCCGTGGGGCCCTGAAGGCCCTTGAAGGCCCTGCTGGGGGCCCTG 300 319 GAGCTGGGTCCCCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGCTGGGGGCCCTG 378 09 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTGCTGCT TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTCGGCGGCG TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAAGCCTGTCGCTGCGCGCTGGAGTCGGCGCG GAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG GAGGCCGGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGGTGAAGCTCCTG creaecaeccreaecarcceereaaccaecrearaeaeeereecaeaaerereeer 1 ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGCTCGTGCT CTGAGCAGCCTGGGCATCCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGTGTGGGCT Gaps 0; Length 570; Indels Query Match 99.0%; Score 308.8; DB 9; Best Local Similarity 99.4%; Pred. No. 4.6e-67; Matches 310; Conservative 0; Mismatches 2; A APPLICATION NUMBER: 60/091544

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091626

DR APPLICATION NUMBER: 60/09163

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/09163

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/091982

DR FILING DATE: 1998-07-07

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DR APPLICATION NUMBER: 60/091982

DR FILING DATE: 1998-07-07 FILING DATE: 1998-07-02 ACAGTGTTTGGC 312 Acadrarinade 390 139 121 199 181 259 241 379 79 19 301 PRIOR
PRIOR P ð Db ò 셤 ò 임 ð g ð δ

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Query Match
Best Local Similarity 97.8
Matches 539; Conservative
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Sequence 120, App
Sequence 196114,
Sequence 196114,
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6159.242 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/DS06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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| cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-029-579-120

US-10-027-632-196114

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US-10-027-632-196114

US-10-021-85-6

VS-10-211-858-27

US-10-210-858-27

US-09-989-722-407

US-09-989-727-407

US-09-989-727-407

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US-09-989-727-407
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                                                                                                                      OM nucleic - nucleic search, using sw model
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73	07	442-	163-	604-	456-	721	598	293A		444	181	730	436	687	-734	9-	9	-428	9-	-43	-56	-711	-7	-1.5	-43	-15	-514	-57	-172	-72	
-686-	Φ	-066-	-991-	-866-	S.	-989-	-992-	-989-	-989-	-066-	99	-686-	-066-	-993-	-989	-99	g	-997	-99	-99	066-6	066-6	9-989	99	9-990	-99	9-997	9-997	-99	-990	
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ALIGNMENTS

seq19plus12.rnpb

QY 250 AGCGAAGGTGCGGGCCTCGCGGAGACAAAGGCCGGGCCTGCCT		Db 1110 AGAAGCCTCGTGGCCTTGCCCGGGCAGCTCCCCGCGCGCCCCGCGC 1169 Qy 550 CC 551 Db 1170 CC 1171	RESULT 3 US-10-027-632-196114/c ; Sequence 196114, Application US/10027632 ; Publication No. US20020198371A1 ; GENERAL INFORMATION:	; AFFLICANT: Wang, David G. ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide ; TITLE OF INVENTION: Polymorphisms in the Human Genome ; FILE REFERENCE: 108827.129 ; CURRENT APPLICATION NUMBER: US/10/027,632	CURRENT FILING DATE: 2002-04-30	Query Match 25.5%; Score 143.6; DB 13; Length 533; Best Local Similarity 94.8%; Pred. No. 1.4e-24; Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 1 CGGCGGGGAGGCGGGAGTGAGGCCTGATCGTCCCTGGGCCTCACCTCCCCAGG	Oy 61 CGCAGAAGGCCCACGAGGACCCCAGTGCCCTGGCGCCTCCCCAGG 130 Oy 61 CGCAGAAGGCCCACGAGGACCCCCAGTGCCCGAGGTTGCAGGCTCTGGGATCAGAGG 120 Db 129 CGCAGAAGGCCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTTTGGGATCAGAGG 70 Oy 121 CA-GGGACCAGGGACCCGCCCCCCCCCCCCCCCCCCCCC
• • • • • • • • • • • • • • • • • • •	NGAGGGAAGCTCCCTCACCGGGCCAGCCTG-AGGGGGGCGCGTGGGGTC AAGCGAAGCTGCGGGGTGGGCTTGCGGAAAAAGGCCGGGCCTTGC	361 361 357 421	417 AGCGGAGCGGGCAGGCCTTTCTCAGGAGCGGGGCGAGGCGGGCG	Qy 541 GCCCCGCGC 551 Db 537 GCCCCGCGCC 547	REBULT 2 US-10-059-579-120 Sequence 120, Application US/10059579 Publication No. US20030138783A1 GENERAL INFORMATION: APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE APPLICANT: EVRON, Blla APPLICANT: BVRON, Blla APPLICANT: BVRON, Mary Jo. APPLICANT: PACKLER, Mary Jo. TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY FILE REFERENCE: JUHJ630-1 CURRENT APPLICATION NUMBER: US/10/059,579 CURRENT APPLICATION NUMBER: US/10/059,579 PRIOR PAPLICATION NUMBER: US 09/771,357 PRIOR APPLICATION NUMBER: US 09/771,357 PRIOR PLING DATE: 2001-01-26 NUMBER OF SEQ ID NOS: 136 SEQ ID NO 120 LENGTH: 1794	CRGANISM: Homo sapiens FEATURE: NAME/KEY: misc feature LOCATION: (3597 (359) CHER INFORMATION: n is any nucleotide US-10-059-579-120	Query Match 60.1%; Score 338.4; DB 15; Length 1794; Best Local Similarity 97.8%; Pred. No. 5.7e-70; Americal Similarity 17.8%; Matches 354; Conservative 0; Mismatches 6; Indels 2; Gaps 1; Qy 190 GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGACGGGGGCGCCTGAGGGGGCGC-TGGGGGGCGC-TGGGGGCGC-TGGGGGCGCAA 869 249 .pb 812 GAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGACGGGGGCGC-TGGGGTCAAACGCGAA 869

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69 CACGGGACCAGGAACTGCGCCCCC---CGCCCTGCCTGGCGCA-GGAAGC 14
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE SEPERAGOR: 108927.129
CURRENT PILING DATE: 2002-04-30
CURRENT FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-2
PRIOR FILING DATE: 2000-04-2
PRIOR FILING DATE: 2000-04-2
PRIOR FILING DATE: 2000-04-2
PRIOR FILING DATE: 2000-04-2
PRIOR FILING DATE: 1000-03-29
PRIOR FILING DATE: 1000-03-29
PRIOR FILING DATE: 1900-03-29
PRIOR FILING DATE: 1999-09-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-08
PRIOR FILING DATE: PARESEQ for Windows Version 4.0
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Sequence 6, Application US/10237435
Publication No. US20030124580A1
Seberation No. US20030124580A1
APPLICANT: Walker, Michael G.
APPLICANT: Spiro, Peter A.
APPLICANT: Mirry, Lynn E.
TITLE OF INVENTION: LUNG SURFACTANT MOLECULES
FILE REPERENCE: PP=0019 US
CURRENT APPLICATION NUMBER: US/10/237,435
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                        Sequence 196114, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
                                                          180 TCCCTCACCNG 190
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ORGANISM: Human
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APPLICANT: Bernstein, Jeanne
APPLICANT: Rotem Sorek
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 26083
CURRENT APPLICATION NUMBER: US/10/426,002
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
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                                                                                                                                                          FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030124580Al 242745.1
US-10-237-435-6
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                                                                                                                                                                                                                                                         20.6%; Score 116; DB 15;
100.0%; Pred. No. 3.7e-18;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/317,822
PRIOR FILING DATE: 09-07-2001
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL PROGRAM
SEQ ID NO 6
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20040101876A1
GENERAL INFORMATION:
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; Sequence 27, Application US/10211858
; Publication No. US2030211096A1
; GENERAL INFORMATION:
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SEQ ID NO 18

LENGTH: 527

TYPE: DNA

ORGANISM: HOMO Sapiens

US-10-426-002-18
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Bernstein, Jeanne
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Wasserman, Alon
Hermesh, Chen
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Freilich, Shiri
Beck, Nili
                                                                                                                                                                                                                                                                                               Matches 116; Conservative
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APPLICANT: Xie, Hanging
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Best Local Similarity
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Best Local Similarity
Matches 87; Conserv
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US-10-426-002-18
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Watanabe, Colin K.
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Smith, Victoria
Stone, Donna M.
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Pitti, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78; Conservative
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US-10-210-951-27
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Best Local Similarity
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CURRENT APPLICATION NUMBER: 105.10/211,858
CURRENT FILING DATE: 2002-08-02
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PRIOR FILING DATE: 1966-04-01
PRIOR FILING DATE: 1966-04-01
PRIOR FILING DATE: 1966-09-23
PRIOR FILING DATE: 1996-09-23
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059121
PRIOR PELING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR PELING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/06307
PRIOR APPLICATION NUMBER: 60/06307
PRIOR APPLICATION NUMBER: 60/06305
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
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Publication No. US20030170228A1
GENERAL INFORMATION:
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Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
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Wood, William I.
                                                            Hillan, Kenneth J
Marsters, Scot A.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
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Marsters, Scot A.
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Best Local Similarity 100.
Matches 78; Conservative
                                                                                                                                                                                  Stone, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-858-27
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LENGTH: 569
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                                                                          FILE REFERENCE: P2931RICH
CURRENT APPLICATION NUMBER: US/10/210,951
CURRENT APPLICATION NUMBER: US/10/210,951
CURRENT FILING DATE: 2002-08-02
PRIOR PILING DATE: 2002-08-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1996-09-03
PRIOR PILING DATE: 1997-09-13
PRIOR PILING DATE: 1997-09-13
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PRIOR PILING DATE: 1997-09-13
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-10
PRIOR PAPLICATION NUMBER: 60/06307
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-24
                               APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P2931R1C1
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
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Pred. No.
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Publication No. US20030175900A1
GENERAL INFORMATION:
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Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
Watanabe, Colin K.
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FILING DATE: 1998-06-12
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SEQ 1D NO 27
LENGTH: 569
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100.0%; Pred. No. 2.5e-09;
ive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
           PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR PELING DATE: 1997-07-17
PRIOR PELING DATE: 1997-07-17
PRIOR PELING DATE: 1997-07-19
PRIOR PELING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/06375
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
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Patent No. US20020072067A1
GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
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Wood, William I.
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 FILING DATE: 1996-09-23
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Paoni, Nicholas F.
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Kljavin, Ivar J.
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Eaton, Dan I.
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; ORGANISM: Homo sapiens
US-10-211-884-27
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NR APPLICATION NUMBER: 60/06220

R FILING DATE: 1997-10-17

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R APPLICATION NUMBER: 60/065311

R APPLICATION NUMBER: 60/065311

R APPLICATION NUMBER: 60/066770

R FILING DATE: 1997-11-24

R FILING DATE: 1997-11-24

R FILING DATE: 1998-01-24

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APPLICATION NUMBER: 60/088217
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APPLICATION UNMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089105
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474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCCGCGC 533 1 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCGGGG 60 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG62 Gaps 0; Length 570; 0; Indels Query Match
13.9%; Score 78; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17 DR FILING DATE: 1998-06-26

BR APPLICATION NUMBER: 60/090863

BR FILING DATE: 1998-06-26

BR FILING DATE: 1998-06-26

BR FILING DATE: 1998-07-01

BR FILING DATE: 1998-07-02

BR PILING DATE: 1998-07-02

BR PLING DATE: 1998-07-02 RESULT 11
US-09-989-723-407
Sequence 407, Application US/09989723
Sequence WS2005072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J. APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. 534 GCCCCGAGCCCCCGCGCC 551 Paoni, Nicholas F.
Roy, Margaret Ann
Scowart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Zhang, Zemin decedendedecededede 78 Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Gerritsen, Mary E. Fong, Sherman Gerber, Hanspeter Kljavin, Ivar J. Napier, Mary A. Baker, Kevin P. Botstein, David Goddard, Audrey Pan,James 61 APPLICANT:
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NUMBER: 60 1997-11-1 NUMBER: 60 1997-11-2 NUMBER: 60 1998-02-2 NUMBER: 60 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-05-2	1998-06-0 NUMBER: 60 NUMBER: 60 NUMBER: 60 1998-06-0 NUMBER: 60	1998-06-05 1998-06-05 1998-06-05 NUMBER: 60/08821 1998-06-05 1998-06-05 1998-06-00 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08873 1998-06-10 NUMBER: 60/08881 1998-06-10 NUMBER: 60/08881 1998-06-10 NUMBER: 60/08882 1998-06-10 NUMBER: 60/08882 1998-06-10 NUMBER: 60/08882 1998-06-10 NUMBER: 60/08886 1998-06-10 NUMBER: 60/08886 1998-06-10 NUMBER: 60/08886 1998-06-11 NUMBER: 60/08887 1998-06-11 NUMBER: 60/08887 1998-06-11 NUMBER: 60/08897 1998-06-11 NUMBER: 60/08897 1998-06-11 NUMBER: 60/08897 1998-06-11 NUMBER: 60/08997 1998-06-11 NUMBER: 60/08997 1998-06-11
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R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
R PELLING DATE: 1997-11-24
R APPLICATION NUMBER: 60/079945
R APPLICATION NUMBER: 60/078910
R APPLICATION NUMBER: 60/08332
R FILING DATE: 1998-04-28
                 PRIOR APPLICATION NUMBER: 60/066710
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/08460
PRIOR PILING DATE: 1998-06-27
PRIOR PELLING DATE: 1998-06-27
PRIOR PILING DATE: 1998-06-27
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Alangy Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PS730PICG5
CURRENT APPLICATION NUMBER: US/09/989,279
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-01-17
PRIOR FILING DATE: 1997-1-12
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Patent No. US20020072496A1
GENERAL INFORMATION:
                                                                                    APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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                      FILING DATE: 1998-07-01
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
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Matches 78; Conservative
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APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: 60/08950

PRIOR APPLICATION NUMBER: 60/08991

PRIOR APPLICATION NUMBER: 60/08991

PRIOR PILING DATE: 1998-06-18

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1665
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13.9%; Score 78; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-11.19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PLILING DATE: 1997-06-16
PRIOR PLILING DATE: 1997-01.17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11.12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
PRIOR PLILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06531
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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Patent No. US20020072497A1
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Gurney, Austin L.
Kljavin
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Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Ferrara, Napoleone
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Napier, Mary A.
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Botstein, David
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US-09-989-727-407
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
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PRIOR PELICATION NUMBER: 60/08950
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PRIOR PELING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/09055
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25

APPLICAL-A-PILING DATE: 1998-06-20
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
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APPLICANT: Tumas, Daniel
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: William I.
APPLICANT: Second of Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBENCE: P273901C70
CURRENT APPLICATION NUMBER: 126/09/989,731
CURRENT FILING DATE: 2001-11-20
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13.9%; Score 78; DB
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 78; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR PEDISTANCE OF THE TRIES 
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FLING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062150
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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R APPLICATION NUMBER: 60/066770
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R APPLICATION NUMBER: 60/078910
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Botstein, David
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US-09-989-731-407
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PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-16
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PRIOR PRIOR PAPLICATION WUMBER: 60/089512
PRIOR PILING DATE: 1998-06-16
APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088655
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089599

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PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR APPLICATION NUMBER: 60/090678
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 60/089947 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 60/090445 009680/09 60/089952 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090252 60/090254 60/090349 60/090355 APPLICATION NUMBER: 60/090429 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 60/090472 APPLICATION NUMBER: 60/089653 60/090431 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24 1998-06-17 1998-06-17 FILING DATE: 1998-06-22 1998-06-22 FILING DATE: 1998-06-23 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ 1998-06-17 1998-06-23 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: FILING DATE: PRIOR

533 APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acide Encoding the Same FILE REFERENCE: P2730PLC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT PELING DATE: 2001-11-19
PRIOR PRILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06230
PRIOR APPLICATION NUMBER: 60/065136
PRIOR APPLICATION NUMBER: 60/065136
PRIOR PILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR APPLICATION NUMBER: 60/092182 Sequence 407, Application US/09989732 Patent No. US20020123463A1 13.9%; Scur. 100.0%; Pre APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/066770 PRIOR FILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/075945 PRIOR FILING DATE: 1998-02-25 Godowski, Paul J. Grimaldi, J. Christopher 534 GCCCCGAGCCCCCGCGCC 551 61 GCCCCGAGCCCCCGCGCC 78 Watanabe, Colin K. Williams, P. Mickey Wood, William I. Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Ferrara, Napoleone Gerritsen, Mary E. Fong, Sherman Gerber, Hanspeter Gurney, Austin L. Kljavin, Ivar J. Query Match 13.9 Best Local Similarity 100. Matches 78; Conservative APPLICANT: Ashkenazi, Avi J. Botstein, David Goddard, Audrey Napier, Mary A. Baker, Kevin P. Desnoyers, Luc Eaton, Dan L. Pan, James GENERAL INFORMATION: RESULT 15 US-09-989-732-407 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT PRIOR PRIOR PRIOR PRIOR à 임 ð

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PRICES APPLICATION NUMBER: 60/089948
PRICES PLILING DATE: 1998-06-29
PRICES PLILING DATE: 1998-06-29
PRICES PLILING DATE: 1998-06-29
PRICES PLILING DATE: 1998-06-23
PRICES PLILING DATE: 1998-06-24
PRICES PLILING DATE: 1998-06-25
PRICES PLILING DATE: 1998-06-26
PRICES PLILING DATE: 1998

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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1996-07-07
PRIOR PRIOR TOWN NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels

0; 474 GCCAGGACCGGGTALAAGAAGCCTCGTGGCCTTGCCCGGGCAGCTTCCCCGCGC 533

> ò Dp

534 GCCCCGAGCCCCCGCGCC 551

61 GCCCCGAGCCCCCGCGCC 78

qq ð

Search completed: June 6, 2004, 19:49:10 Job time : 417 secs

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Sequence 2, Appli
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Sequence 10, Appl
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Sequence 1, Appli
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-08-843-659-1
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US-08-306-691B-14
US-09-209-668-10
US-09-356-952-B
US-08-232-463-14
US-09-616-289-45
US-09-6690-473-1
US-09-616-289-45
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US-09-103-840A-1
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PCT-US91-06532-1
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Listing first 45 summaries
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Waximum DB seq length: 200000000
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Match Length DB
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36,	sequence 36, Appl Sequence 1, Appli	- -1	٦,	m	651	Sequence 6520, Ap	Sequence 17202, A	Sequence 6540, Ap	Sequence 1, Appli	H	H	H	Sequence 2, Appli	, ,	121	H
US-08-483-533-36	US-U9-Z83-4/LA-36 PCT-US91-06532-1	US~09-105-537-1	US-09-091-609-1	US-09-091-609-3	US-09-252-991A-6511	US-09-252-991A-6520	US-09-621-976-17202	US-09-252-991A-6540	US-08-091-569-1	US-08-203-676-1	US-08-822-238-1	US-08-785-420-1	US-08-658-136-2	US-08-658-136-1	US-09-023-655-1215	US-08-572-951-1
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45.4	45.4	45.4	45.4	45.4	45	45	44.2	44.2	44	44	44	44	43.8	43.8	43.6	43.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 GCAGGGGGGGCGCGTGGGGGTCAGACCGCAAAGCGGAAGGTGCGGGGCCGGGGTGGGCCTCGCG
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Patent No. 6117654
Batent No. 6117654
Batent No. 6117654
TITLE UFORMATION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-00-03
EARLIER FILING DATE: 1998-00-02
EARLIER PLING DATE: 1998-00-02
EARLIER PLING DATE: 1998-00-03
EARLIER PLING DATE: 1998-00-04
MINMER OF SEC IN NOW. 1907-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 50.8; DB 3; Length 152331;
48.7%; Pred. No. 0.035;
tive 0; Mismatches 173; Indels 3;
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 18
SOFTWAREE FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.7
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
US-09-128-155-16/c
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                                                                    Score 49.4; DB 5; Length 1
Pred. No. 0.056;
0; Mismatches 182; Indels
521 AGGITCCCCGCGCGCCCCGAGCCCCCGCCGGCCGGGGAGG 563
                                                                                                                                                                  RESULT 2
PCT-0591-0532-1/c
PCT-0591-06532
Sequence 1, Application PC/TUS9106532
GENERAL INFORMATION:
PAPPLICANT: Roizman, Bernard
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses
TITLE OF INVENTION: Vaccines and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06532
FILING DATE: 19910910
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two First National Plaza Suite 2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEFAX: 312/984-9740
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 48.0%;
Matches 169; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
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CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR PELICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                             RESULT 3
US-09-616-289-48/c
; Sequence 48, Application US/09616289
; Patent No. 6632923
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; Patent No. 6632>2.
; GENERAL INFERMATION:
; APPLICANT: Lees, Robert S.
''nT.ICANT: Lees, Robert S.
''nav, Simon F.
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                                                                                                    Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: PRASEX:
Claire M.
APPLICANT: PRASEX:
Claire M.
APPLICANT: PRASEX:
Claire M.
APPLICANT: APPLICANT: PRASEX:
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBRECULOSIS
TITLE OF INVENTION: TUBRECULOSIS
TITLE OF INVENTION: 13466-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN OF 2.1
                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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Pred. No. 0.1;
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TYPE: DNA
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481
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Sequence 1, Application US/09103840A

Sequence 1, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILLE REPRESENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1
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47.9%; Pred. No. 0.13;
tive 0; Mismatches 247; Indels 11;
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HERPES SIMPLEX VIRUS ICP4 AS
INHIBITOR OF APOPTOSIS
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OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Patent No. 5876923
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APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SI
TITLE OF INVENTION: INHIBITON
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TYPE: DNA ORGANISM: HERPES VIRUS, TYPE
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          GENERAL INFORMATION:
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US-08-843-659-1/c
                                                                                                                                                             SEQ ID NO 1
LENGTH: 4257
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                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-JUL-1996
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 GCCCCGAGCCCCCGCGCCGGCCG 557
                              ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 4257 base pairs
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Matches 210; Conservative
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                 ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                             FILING DATE: 26 CLASSIFICATION:
                                                          Houston
                                                                          Texas
                                                                                 COUNTRY: US;
ZIP: 77210
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                                                        CITY: F
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RESULT 7 18-09-259-821A-1/c 5 Sequence 1, Application US/09259821A 5 Patent No. 6210926

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APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REFERENCE: ARCD:317
CURRENT APPLICATION NUMBER: US/09/259,821A
PRIOR APPLICATION NUMBER: 09/690,473
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-07-26
SOFTWARR: PARCH DATE: 206-07-26
SOFTWARR: PARCH DATE: 21.1
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Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Loopardi, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 6
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Pred. No. 0.1;
0; Mismatches 229;
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Texas
COUNTRY: United States
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Philadelphia
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APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48.2; DB 3; Length 4257;
Pred. No. 0.1;
0; Mismatches 229; Indels 5
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                 APPLICATION NUMBER: US/08/843,659
FILING DATE: CONCURRENTLY Herewith
CLASSIPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%;
                                                                                                                                                                                                                                                                                 TELFFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.3
Matches 210; Conservative
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STRANDEDNESS: single
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STREET: On
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US-08-458-568A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.6%; Score 48.2;
47.3%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Herpes simplex virus STRAIN: Herpes Simplex Virus Type 1 US-08-458-568A-11
                                                                               SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-UUNE-1995
                                                                                                                                                                                                                                                                              36,317
ER: DFCI-0029
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 GCCCCGAGCCCCCGCGCCGGCCG 557
                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 36,317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
SEQUENCE CHARACTERISTICS:
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                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                    12001 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 210; Conserv
                                                                                                                                     FILING DATE: 02 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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19103
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                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                      489 AAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCCGCGCCCCCGAGCCCCCGGC 548
         GCTTCCCAGGGCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGTGAGCGGAGC 428
                                                                                                                                                                                                                                                                                                                409 GCCCCGCCCCCCCCCCCCTCCGCCAGCCCCGCCCTACCATTGCCTGCGCCCATCGG 350
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                                                                                                                                GGGCAGGGCTTTCTCAGGAGCGCGGGGGGCCGGCGCTGGAGGGGGGGAGGACCGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
CURRENT PPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
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8.4%; Score 47.4; DB 3;
Best Local Similarity 46.5%; Pred. No. 0.15;
Matches 255; Conservative 0; Mismatches 287;
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: V00574/Genbank
DATABASE ENTRY DATE: 1991-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09209668A Patent No. 6114517
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(1664)..(1774)
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(2042)..(2220)
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ORGANISM: Homo sapiens
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FEATURE:
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                                                   Sequence 14, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION
APPLICANT: CALAbretta, Bruno
APPLICANT: SKOTSKi, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCES: 55
CORRESPONDENCES Seidel, Godda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19102
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
~merTTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MODACO, Daniel A. ERGISTRATION NUMBER: 30,480
REFERRINCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 14:
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(215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6453 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 6453 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: Septembe
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Penn Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
RESULT 10
US-08-306-691B-14/c
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TELEFAX: (2
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US-08-306-691B-14
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APPLICANT: Laufer, Edward M.
APPLICANT: Dazco, Olivia E.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Fringe Proteins and Pattern Formation
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICATION NUMBER: US/08/586,165
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larity 47.7%; Pred. No. 0.16;
Conservative 0; Mismatches 183;
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NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-05
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Cole, Philip
APPLICANT: Kurjan, John
APPLICANT: Kurjan, John
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Nurber (Cole, Philip)
APPLICANT: Cole, Philip
ACKPSTRING: 600-1-28 M
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
FEARLIER FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHILIN VEY: 2.0
                                                                                                                                                                                                                                      309 GAGGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGGGAACGG
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; ORGANISM: Homo sapiens
US-09-356-952-8
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	463-14/C = 14, Application US/08232463 C0.567037 CCANT: SCHIFLINGER, F. CCANT: SCHIFLINGER, F. CCANT: SCHIFLINGER, F. GCANT: SCHIFLINGER, F. GCANT: SCHIFLINGER, F. GCANT: SCHIFLINGER, F. GOF INVENTION: RECOMBINANT FOWIDED SEPONDENCE ADDRESS: SSPONDENCE ADDRESS: SSSPONDENCE BOOK SOUTH STATE STATION SYSTEM: FOR ADDRESS: SSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSPONDENCE ADDRESS: SSSSSPONDENCE ADDRESS: SSSSSSPONDENCE ADDRESS: SSSSSSSSPONDENCE ADDRESS: SSSSSSSPONDENCE ADDRESS: SSSSSSSPONDENCE ADDRESS: SSSSSSSSSSPONDENCE ADDRESS: SSSSSSSSSSPONDENCE ADDRESS: SS	Similarity 4.4%; Pred. No. 0.17; 3; Conservative 171; Mismatches 114; Indels

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EWRA cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
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Drosophila melanogaster genome survey sequence T7 end of BAC

BACKISENIO of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                   /clone="CSOCAPO04YI20"
/tissue type="THYMUS"
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/note="Vector: pcMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and cloned ithe Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized."
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
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Llarity 32.5%; Pred. No. 0.00022;
Conservative 100; Mismatches 211;
                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/do xxef="taxon:966"
/clone="CSOCAPONYI20"
/tissue_type="THYMUS"
/tissue_type="THYMUS"
/clone_lib="Homos sapiens THYMUS"
/note="Vector: pWNVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI and cloned into the Not I and EOCRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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BX415111 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP004Y120
5-PRIME, mRNA sequence.
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library Library i Flangal Email: Flangal@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO04BE10QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 CGSGSSSSCCCCSGGSGSCSGGCSSSGSSCCCCCCG--GGSCSCSSSSSCCCSCCSGG
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 982)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                           / Match 15.7%; Score 88.4; DB 13;
Local Similarity 32.3%; Pred. No. 1.9e-05;
nes 142; Conservative 114; Mismatches 182;
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BX415111.1 GI:30765470
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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SOURCE

368

428 459 488 519

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"Web: www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila denome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG032885 11313 bp DNA linear GSS 01-NOV-2001.
Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.
AG032885
                   BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCCAGCGCCT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 GCCAAGAAGTACTCCACGAGGCCCGGGGAAAGGGGGGCACGGGGCTTCCCAAGGGCCCGG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_txref="taxon:7227"
/clone="BACR14N09"
/clone=lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81.2; DB 29;
Pred. No. 0.00032;
2; Mismatches 173;
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                        Pujiyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission

Direct Submission

Bibmitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel.81-45-503-9111, Fax:R81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
priMERS
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 0.00051;
0; Mismatches 301;
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/mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-007M05.F"
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                  BAC end sequences of Library PTB Unpublished
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: SacI.
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/note="Vector: pBluescript II SK-; Site I: ECORI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines consa cc-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PO17M mRNA was purified from each sample, pooled and CDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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Strain="CC-1690 wild type mt+ 21gr"
(db_xref="taxon3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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(Chamydomonadaceae; Chlamydomonas.

(Tobase 1 to 1281)

Grosman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.

McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.

Manjese of the Chlamydomonas reinhardtii Genome: A Model,
Unicallular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2

Unpublished (2000)

Contact: Charles Hauser

DCMB Box 91000

Duke University
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/clone="IMAGE:572F629"
/tissue_type="hippocampus"
/lab_host="DH108"
/clone lib="MIH MGC 124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source male hippocampus, age_27. Library is oligo-df primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA linear EST 20-FEB-2002 sapiens cDNA clone IMAGE:5727629
CTCTCTCAG--AGGGCCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCCGGGCAGGGAA 358
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1 (Dases 1 to 1284)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                  GGGGGCACGGGCTTCCCAGGGCCCCGCCGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCG
                                                                                                                                                                       GACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGCCCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: Limage.llnl.gov
High quality sequence stop: 249.
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AGENCOURT_6507057 NIH_MGC_124 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Homo sapiens"
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db_xref="taxon:9606"
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BMS47577
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Best Local Similarity 45.6
Matches 259; Conservative
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CGGCCGGGGGGGGGGGGGGGGCCTGATCGTCCCTGGCGCCTCCACCTCCCAGG

0; Mismatches 303; Indels

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"Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila genome Project (BDCP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Coogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19016 of RPCI-98 library from Drosophila melanogaster (fruit AL053013
                                                             1040
CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG 120
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                             GAAGCTCCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCTGCCTGCAGGGGGGGCGCGT
                                                                                                                                                                                                                                                                                                                           GGGGTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCCTCGCGGAGACAAAGGCCCGG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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Gaps

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Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobACII.
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                                                                                                                                                                                                                                                                                                                     238 GTCAGACCGCAAAGCGAAGGTGCGGGCCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGGC 297
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http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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                                                            melanogaster<sup>1</sup>
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llarity 13.3%; Pred. No. 0.0015;
Conservative 185; Mismatches 128;
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                                                                          /mol_type="genomic DNA"
/db_xref="taxon.7227"
/clone="bacR19D16"
/clone lib="RPCT-98"
/note="end : TET3"
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                                                          /organism="Drosophila
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Best Local Similarity
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DEFINITION
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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                                                                                                                                                                                                                                                                                                                       695 ASCACMAADCGGCCAKMACCSSSASSSGSSCASTSSSASKGGMVSSCACSGSGGGASA
                                                                                                                                                                                                                                                   635 ACACGGSAGCGGRRKGCAACKSAGMSSCGGRSGSGSSCCCGGKKAKGGVRGGRVCCAGGG
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                          Length 1101;
                                                                                                                                                                                           Indels
 melanogaster"
                                                                                                                                                        13.5%; Score 75.8; DB 29;
llarity 15.8%; Pred. No. 0.0028;
Conservative 216; Mismatches 151;
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                /mol_type="genomic DNA"
/db xref="taxon:7227"
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/organism="Drosophila
                                                  /clone="BACN37L08"
/clone lib="DrosBAC"
/plasmid="pBelcBAC11"
/note="end : SP6"
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Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J. An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1173 GÓCGCCGGCCGGCCCCGGCCGCCCNCGGCGCCCCCCGCGGCCGGGGCCGCGCGCGCGCG 1232
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/clone_lib="Ppa EcoRI BAC Library"
hote="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1628
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                                                                                                                             Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Speannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                             (2003)
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Pred. No. 0.0049;
0; Mismatches 285;
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                                                                                                                                                                                                                                            Email: ralf.sommer@tuebingen.mpg.de Class: BAC ends.
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
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               Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Aaron Mammoser in Pieter de Jong's laboratory in the Department
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Neodiplogasteridae; Pristionchus.
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
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/clone="BACR14B09"
/clone_lib="RPCI-98"
/note="end : T7"
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Submitted (02-A05-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-021N08.F, genomic survey sequence.
AG043499
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                              67 AGGCGCCCACGAGGACCCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGGCAGGGA
                                                                            127 CCAGGGAGCCAGGAACTGCGCCGCCCCGCCCTGCCCTGGCGCGAGGGAAGCTCCCTCA
                                                                                                                                                                                  247 CAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGCTCTCT
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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Pan troglodytes
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GOCCCCAGGGCCTGCCAAGAGGAAGTCCTCGAGGCCCCGGGCAGGGAAGGGGCCACGGGCT 371
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Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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0; Mismatches 292; Indels
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/oell_type="primary mesenchyme
/lab_host="E.coli"
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/clone="PC_0028_A2_G12_MR"
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Zhu,X., Mahairas,G., Illies,M.R.,
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Carnegie Mellon University
4400 Fifth Avenue, Pittsburgh,
Tel: +1 412 268 5849
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BG786331.1 GI:14157344
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Matches 261; Conservative
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sex="male"
'cell_type="lymphoblast"
'clone_lib="PTB Chimpanzee Male BAC Library"
1. .949
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     source
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2; 57 CAGGCGCCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCA 116 117 GAGGCAGGAGCCAGGAACTGCGCCCCCCCCCCCTGCCCTGCCGAGGGA 176 177 AGCTCCCTCACCNGAGGGAAGCTCCCCTCACCCGGCCCAGCCCTGCAGGGGGGGCGC---- 232 233 ---GTGGGGTCAGACCGCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAG 289 Gaps 6 Score 73.6; DB 29; Length 949; Pred. No. 0.0064; O; Mismatches 267; Indels 9 Query Match
Best Local Similarity 44.9%;
Matches 225; Conservative (849 789 ò CD qq à à

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470 AGGGGGGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGGAGCCGCAGGTTCCCC 529

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(without alignments) 5890.974 Million cell updates/sec

SEQ19PLUS12 563 Title:

1 cggccggggaggcggccggg........... Perfect score: Sequence:

563

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseg 29Jan04: Database :

1: geneseqn1990s:*
2: geneseqn1990s:*
4: geneseqn2001as:*
5: geneseqn2001as:*
6: geneseqn2002s:*
7: geneseqn2002s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003cs:* geneseqn2003as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:

SUMMARIES

Re

Description	Abt06542 Human HIN	0	6 LU105	Ade39936 Human lun	Aaz29723 Human lun	Aaz98173 Human siq	Aav54621 LU105 pol	Abk40267 cDNA enco	Aaz65103 Membrane-	Aaf44249 Human PRO	Abx77974 Human PRO	Abx80386 Novel hum		Abx90363 Human sec	Abx64209 cDNA enco	Aca64431 Novel hum	Abx80890 Human sec	Acd44399 cDNA enco	Abx79570 Human sec	Aca93591 Novel hum	Abx81273 Novel hum		Abx17173 Human PRO
ID	ABT06542	AAV54620	AAV54616	ADE39936	AAZ29723	AAZ98173	AAV54621	ABK40267	AAZ65103	AAF44249	ABX77974	ABX80386	ACA69292	ABX90363	ABX64209	ACA64431	ABX80890	ACD44399	ABX79570	ACA93591	ABX81273	ACA93089	ABX17173 ·
DB	9	7	7	6	m	m	7	9	m	Ŋ	7	7	7	7	7	7	7	7	7	7	7	7	7
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Score	298.4	120	117	116	92	92	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78	78
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Aca68028 Novel hum	Aca88477 Human sec	Acd81984 cDNA enco	Ada37918 Human cDN	Ada21604 Human cDN	Ada10391 Human cDN	Ada17935 cDNA enco	Ada28043 Human cDN	Ada94623 Human cDN	Ada38848 Human cDN	Ada92969 Human cDN	Ach65545 Human cDN	Ada22530 Human cDN	Acd39535 Human cDN	Ada06696 Human sec	Ada39389 Human CDN	Adb96415 Human PRO	Adc57887 Human PRO	Adc55251 Human PRO	Adc12118 Human cDN	Adc56540 Human PRO	Adc07595 Human cDN
8 ACA68028	8 ACA88477	8 ACD81984	8 ADA37918	B ADA21604	8 ADA:10391	8 ADA17935	B ADA28043	8 ADA94623	8 ADA38848	B ADA92969	8 ACH65545	8 ADA22530	8 ACD39535	8 ADA06696	B ADA39389	8 ADB96415	9 ADC57887	9 ADC55251	9 ADC12118	9 ADC56540	9 ADC07595
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. 24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

gene; hypermethylation; Human; methylated gene; methylation; breast cancer; marker; WT-1; cell prollferative disorder; WTST; MVRSF, MSS-1; RARbeta; cyclin D2; retinoic acid receptor beta; cestrogen receptor; Wilms' tumour; 14.3.3 sigma; HIN-1; RASSFIA, tumour suppressor gene; hypermethylation BP. ABT06542 standard; DNA; 1794 Human HIN-1 coding sequence. (first entry) gene; promoter; ds 07-NOV-2002 ABT06542; ABT06542

28-JAN-2002; 2002WO-US002455. WO200259347-A2, Homo sapiens 01-AUG-2002.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

26-JAN-2001; 2001US-00771357.

Fackler MJ Davidson N, Sacchi N, Dooley WC, Evron E, Sukumar S,

λą Diagnosing and/or determining a predisposition to a cellular proliferative disorder of breast tissue, in particular breast cancer, determining the state of methylation of one or more nucleic acids isolated from the subject WPI; 2002-599803/64.

Disclosure, Fig 9A, 115pp, English.

The present invention relates to a method of diagnosing a cellular proliferative disorder of breast tissue, which involves determining the state of methylation of one or more nucleic acids isolated from the subject, where the state of methylation of the nucleic acids as compared with a state of methylation from a subject not having the cellular proliferative disorder of breast tissue is indicative of a cellular proliferative disorder of breast tissue in the subject. The nucleic acids

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1085
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may be TWIST, HOXA5, NES-1, retinoic acid receptor beta (RARbeta), oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma, HIN-1 or RASSFIA. The method is useful for diagnosing and/or determining a predisposition to a cellular proliferative disorder, in particular breast cancer including ductal carcinoma in situ, lobular carcinoma, colloid carcinoma, medillary carcinoma, metaplastic carcinoma, intraductal carcinoma, medillary carcinoma, metaplastic carcinoma in situ. The present sequence is a gene fragment used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906 AAAGGCCGGGCCTGCCTCTCTCAGAGGGCCCCAGGCGCCTGCCAAGAGGAAGTCCTCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                    846 GGGGGCGCTGGGGTCAGACCGCAAAGCGAAAGTGCGGGCCGGGGTGGGGCTCGCGGAAAA
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                            Length 1794;
                                                                                                                                                                                                                  Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 0 U; 68 Other;
                                                                                                                                                                                                                                                                                                 Indels
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/product= "LU105 polypeptide"
                                                                                                                                                                                                                                                     Score 298.4; DB 6;
Pred. No. 1.6e-48;
0; Mismatches 24;
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/transl_except=
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                                                                                                                                                                                                                                                          Query Match 53.0%;
Best Local Similarity 92.6%;
Matches 302; Conservative
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(first entry)
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30-OCT-1998
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Sequences shown in AAV54616 to AAV54621 represent LU105 specific polymucleotide sequences. These are used in the method of the invention for detecting target LU105 nucleic acid. The method comprises treating a sample with at least one LU105 specific nucleic acid, or its complement which is at least so percent identical with the LU105 specific nucleic acid sequences (AAV54616 to AAV5461). LU105 is a lung disease marker.

Cells transformed with a recombinant expression system that contains LU105 specific nucleic acid fragments, are used to express recombinant LU105 polypeptides which are used to raise antibodies. The antibodies are used to detect the LU105 antipodies, in usual immunoassays. The LU105 polypeptides and nucleic acid sequences are used for diagnosis, staging, monitoring, prognosis, prevention, treatment and determination of polypeptides are also used to screen for specific binding agents, useful therapeutically, LU105 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment). LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                              nucleic acid for the lung disease marker LU105 - polypeptides, bodies and genes, used for diagnosis, prevention, treatment of lung
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       Cohen M, Colpitts TL, Friedman PN, Gordon J; ss SC, Klass MR, Kratochvil JD, Robertsrapp L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 0 U; 2 Other;
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Pred. No. 2.8e-14;
0; Mismatches 1;
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disease, specifically cancer.
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Billing-Medel PA, Cohen P
Granados EN, Hodges SC,
Pussell JC, Stroupe SD;
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                                                                              WPI; 1998-437479/37.
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                                                                                                 P-PSDB; AAW75868
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30-OCT-1998
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97US-00791710

31-JAN-1997;

of for

for detecting target LU105 nucleic acid. The method of the invention for detecting target LU105 nucleic acid. The method comprises treating a sample with at least ton EU105 specific nucleic acid. Or its complement which is at least 50 percent identical with the LU105 specific nucleic acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker. CC calls transformed with a recombinant expression system that contains LU105 specific nucleic acid fragments, are used to express recombinant cut used to obtain the nucleic acid fragments, are used to express recombinant cut used to detect the LU105 antibodies. The antibodies are used to detect the LU105 antibodies, in usual immunoassays. The LU105 polypeptides and nucleic acid sequences are used for diagnosis, staging, cused to detect specific antibodies, in usual immunoassays. The LU105 polypeptides and nucleic acid sequences are used for diagnosis, staging, conjugentially to, lung disease, specifically cancer. The LU105 cusceptibility to, lung disease, specifically cancer. The LU105 cusceptibility to, lung disease, specifically cancer at high concentration, in altered form or in an unusual body compartment). LU105 can be detected in blood, plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.) 431 GCAGGGCTTTCTCAGGAGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAA 490 GAAGCCTCGTGGCCCTTGCCCGGGCAGCCGCAGGTTCCCCGGGGGCCCCGAGCCCCGGGGC 550 GANGCCTCGTGGCCTTGCCCGGGGCAGCCGCAGGTTCCCCGCGCCCCCGANCCCCCGCGCCCTC GCAGGGCTTTCTCAGGNGCGCGGGCGAGGCCGGCGCTGGAGGGGCGAGGACCGGGTATAA 60 New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer. Cohen M, Colpitts TL, Friedman PN, Gordon J; es SC, Klass MR, Kratochvil JD, Robertsrapp L; Sequences shown in AAV54616 to AAV54621 represent LU105 specific 20.8%; Score 117; DB 2; Length 190; 96.7%; Pred. No. 1.1e-13; Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 0 U; 4 Other; Human lung disorder-related cDNA - SEQ ID 6. 0; Mismatches pepsin C; lung disorder; human; ss Claim 11, Fig 1; 123pp; English. ADE39936 standard; cDNA; 561 BP. (first entry) Best Local Similarity 96.7 Matches 117; Conservative Hodges SC, Stroupe SD; WPI; 1998-437479/37 (ABBO) ABBOTT LAB. Billing-Medel PA, US2003124580-A1 ¢ 121 C 551 Granados EN, Russell JC, Homo sapiens 29-JAN-2004 03-JUL-2003 491 61 551 ADE39936 Query Match RESULT 4 ADE39936 셤 à XX XX PA à à g XX XX SO XX

4; Indels

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The invention relates to a novel isolated cDNA and a cDNA encoding pepsin C. The polymucleotide of the invention may be useful as a probe or a component within an expression vector, as a diagnostic in assessing the prognosis and treatment of a lung disorder and as a potential therapeutic or target for the identification of therapeutics for lung disorders. With the polymucleotide may be used to produce purified proteins or peptides which can subsequently be used to produce antibodies. The current sequence is that of the human lung disorder-related cDNA (SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate; lung cancer; diagnosis; ds.
                                                                                                                                        New cDNAs co-expressed with lung surfactant and surfactant synthesis genes, useful as diagnostics in assessing the prognosis and treatment a lung disorder, or as potential targets for identifying therapeutics lung disorders.
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                                                                                                                                                                                                                                                                                                                                                                Sequence 561 BP; 86 A; 200 C; 189 G; 86 T; 0 U; 0 Other;
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                                                                                                                                                                                                        Claim 2; SEQ ID NO 6; 29pp; English.
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                                                                                        Murry LE;
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          06-SEP-2002; 2002US-00237435
                                    07-SEP-2001; 2001US-0317822P
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                                                             (INCY-) INCYTE GENOMICS INC.
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/product= '
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                                                                                                               WPI; 2003-810982/76.
                                                                                                                                                                                                                                                                                                                                        of the invention.
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es 116; Conserv
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                                                                                       Walker MG,
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                                                                                                                                                              The present sequence is a lung specific gene (LSG) Lng107 from human clone ID 566271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cartdiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorgone GA, Corley NC, Guegler KJ, Baughn MR; foung J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGGCCTGGAGGGCGGGGAGGAGCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                  460 CCGGCGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human signal peptide containing protein HSPP-65 cDNA SEQ ID NO:199.
                                                                                         A new method for diagnosing, monitoring and staging lung cancer
                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                    16.3%; Score 92; DB 3; Length 543; 100.0%; Pred. No. 6.7e-09; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 CAGGITCCCCGCGCGCCCCGAGCCCCCGGGCC
                                                                                                                                                                                                                                                              obtained from patient and normal control
                                                                                                                             Claim 6; Page 36; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0090762P.
98US-0094983P.
98US-0102686P.
98US-0112129P.
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscular dystrophy; ss
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P-PSDB; AAY87288.
                                     WPI; 2000-116320/10
Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
                                                      P-PSDB; AAY44458
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Akerblom IE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ98173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP mucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or thosyme therapeutics, for detecting related sequences or genetic minimals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 CCGGCGCTGGAGGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCG 519
                                                                                                                                                                 AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (potential therapeutic agents). Ab are used to diagnose, or monitor, HS -related diseases (in usual immunoassays), as therapeutic antagonists, competitive drug screens, and for purification of HSPP from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGCGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LU105; lung disease marker; immunoassay; lung disease; cancer; blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/transl_except= (pos:136. .138, aa:Val)
/product= "LUI05 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 3; Lu
Pred. No. 6.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520 CAGGITCCCCCCCCCCCCAGCCCCCCCCCCCCC 551
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                                                                                                            Claim 9; Page 289; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US001766.
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(first entry)
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conjuncted tide sequences. These are used in the method of the invention for detecting target LU105 nucleic acid. The method comprises treating a sample with at least boulder acid. The method comprises treating a sample with a teast boulder specific nucleic acid. Or its complement which is at least 50 percent identical with the LU105 specific nucleic acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker. Cells transformed with a recombinant expression system that contains LU105 specific nucleic acid fragments, are used to express recombinant LU105 polypeptides which are used to raise antibodies. The antibodies are used to detect the LU105 antibodies, in usual immunoassays. The LU105 polypeptides and nucleic acid sequences are used for diagnosis, staging, onlypeptides and nucleic acid sequences are used for diagnosis, staging, susceptibility to, lung disease, specifically cancer. The LU105 polypeptides are also used to screen for specific binding agents, useful therapettically, LU105 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment). LU105 can be detected in blood, plasma or serum in an ineadsoning, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer.
                                                                                                                                                                                           Cohen M, Colpitts TL, Friedman PN, Gordon J; es SC, Klass MR, Kratochvil JD, Robertsrapp L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences shown in AAV54616 to AAV54621 represent LU105 specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 1; 123pp; English
     97US-00791710
                                                                                                                                                                            Billing-Medel PA, Cohen
Granados EN, Hodges SC,
Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-437479/37.
                                                                                           (ABBO ) ABBOTT LAB.
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31-JAN-1997;
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., DB 2; Length 519; Indels Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other; 3.2e-06; hes 0; Query Match 13.9%; Score 78; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 78; Conservative 0; Mismatches

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Gaps

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474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGC 533 1 écdaddaddegranaagaagccrcereccrcecceecagccecagerrcccdeec

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RESULT 8 ABK40267

ABK40267;

ABK40267 standard; cDNA; 569 BP.

cDNA encoding human PRO1245 polypeptide. (first entry) 15-JUL-2002

Human; PRC; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; meuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.

WO200153486-Al

26-JUL-2001

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polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agoniets, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                 Hillan KU;
                                                                                                                                                                                                                                                                                                                                                Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                 Gurney AL,
Smith V,
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Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 50; Fig 27; 302pp; English.
                                                    99US-0123972P.
99US-0133459P.
99WO-US012252.
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99US-0151689P.
99WO-US020111.
                                                                                                              99US-0140653P
                                                                                                                            99US-0144758P
                                                                                                                                           99US-0145698P
                                                                                                                                                                                                                99WO-US021090,
99WO-US028313.
             11-FEB-2000; 2000WO-US003565
                                                                                               99US-0140650P
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Wood WI;
                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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Watanabe CK,
                                                                                                                                                                                                                                                                          05-JAN-2000;
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01-DEC-1999
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for treating

533 09 Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immuncadhesin; gene mapping; ss. 474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGGGC 1 eccadeaccederaraacaaccreerecerreceesecadececaderreceese Membrane-bound protein PRO1245 encoding cDNA. 534 GCCCCGAGCCCCCGCGCC 551 61 GCCCCGAGCCCCCCGCGCC 78 AAZ65103 standard; cDNA; 570 (first entry) 05-APR-2000 AAZ65103; RESULT 9 AAZ65103 ò 셤 à

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Gaps

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Length 569;

DB 6;

Score 78;

13.9%;

Query Match

Best Local Similarity 100.0%; Fred. No. 3.2e-06; Matches 78; Conservative 0; Mismatches 0; Indels

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98US-0090678P

98US-0090678P

98US-0090691P

98US-0090694P

98US-0090694P

98US-0090694P

98US-0090694P

98US-0090694P

98US-0090863P

98US-0090863P

98US-0091848P

98US-0091848P

98US-0091848P

98US-009184B

98US-00968B

98US-009781B

98US-009781B

98US-009787B

98US-009797B

98US-009797B

98US-009797B

98US-009797B
  98US-0090557P
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18-AUG-1998;
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18-AUG-1998
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26-AUG-1998
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98US-0087609P-
98US-0087827P-
98US-0088025P-
98US-0088025P-
98US-0088025P-
98US-0088026P-
98US-0088212P-
98US-0089218P-
98US-0089218P-
98US-0089538P-
98US-0090358P-
98US-0090448P-
98US-0090448P-
98US-0090472P-
98US-0090472P-
98US-0090472P-
                                                                    99WO-US012252
                                                                                    02-JUN-1998;
02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
04-JUN-1998;
          Homo sapiens
                           WO9963088-A2
                                                                  02-JUN-1999;
                                               09-DEC-1999
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-70N-1
-70N-1
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                                                                                                                                                                                                     polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO mucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGGGC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGCCAGGTTCCCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                 Watanabe CK;
                                                                                                                                                                                       The invention provides membrane-bound PRO polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%; Score 78; DB 3; Length 570; 100.0%; Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
                                                                                                                            Membrane-bound proteins and related nucleotide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.
                                 Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; cancer; chromosomal mapping; gene mapping;
                               Goddard A, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF44249 standard; cDNA; 570 BP
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990S-0143048P-
990S-014568P-
990S-014622P-
990S-014622P-
990S-0149396P-
990O-015021547-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCCCCGAGCCCCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                   recombinant techniques
(GETH ) GENENTECH INC.
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                                                                            WPI; 2000-072883/06.
P-PSDB; AAY66757.
                               Chen J,
Yuan J;
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17-AUG-1999;
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15-SEP-1999;
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                               Baker K,
Wood WI,
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Matches
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating ancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PRE primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB55154 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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Godowski PJ;
Paoni NF;
Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Berrara N, Rong S, Gerber H, Gerritsen NE, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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100.0%; Pred. No. 3.2e-06;
cive 0; Mismatches 0;
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100.0%; Pr.
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99WO-US028313.
99WO-US028301.
99WO-US0309105.
2000WO-US030911.
2000WO-US000376.
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2000WO-US004914.
2000WO-US005004.
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2000WO-US007377
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Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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06-JAN-2000;
11-FEB-2000;
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22-FEB-2000;
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20-MAR-2000;
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98US-0090444P.

Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.

Homo sapiens

US2003027163-A1

06-FEB-2003

15-NOV-2001; 2001US~00997666

97US-0049787P. 97US-0062250P. 97WO-US020069. 97US-0065186P.	7US-0065311P 7US-0066770P 8US-0075945P	8US-0078910P 8US-0083322P 8US-0084600P	BUS-0087106P BUS-0087607P	BUS-008/603F BUS-0087759F BUS-0087827P	8US-0088025P	BUS-00880285 BUS-0088029P BUS-0088030P
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24 - 70N - 1998; 25 - 70N - 1998; 26 - 70N - 1998; 27 - 70N - 1998; 28 - 70N - 1998; 29 - 70N - 1998; 20 - 70N - 1998;

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23-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998;

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26-AUG-1998; 31-AUG-1998; 16-SEP-1998; 16-SEP-1998;

26-AUG-1998 26-AUG-1998

26-AUG-1998

17-JUN-1998; 17-JUN-1998; 17-JUN-1998; 17-JUN-1998; 18-JUN-1998; 18-JUN-1998; 18-JUN-1998; 19-JUN-1998; 19-JUN-1998; 19-JUN-1998; 22-JUN-1998; 22-JUN-1998; 22-JUN-1998; 23-JUN-1998;

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17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998;

18-AUG-1998) 18-AUG-1998 18-AUG-1998, 20-AUG-1998; 24-AUG-1998;

11-AUG-1998; 11-AUG-1998; 12-AUG-1998;

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vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum, kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
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97US-0062256P

97US-0065311P

97US-0065311P

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98US-0078910P

98US-008122P

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                                                                                                             US2002132252-A1.
                                                                                         Homo sapiens
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04-JUN-1998;
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100.0%; Pred. No. 3.2e-06;
ive 0; Mismatches 0;
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20-DEC-1999; 99WO-USG30091.
56-JAN-2000; 2000WO-USG30011.
11-FEB-2000; 2000WO-USG00376.
11-FEB-2000; 2000WO-USG004414.
22-FEB-2000; 2000WO-USG004414.
24-FEB-2000; 2000WO-USG00414.
24-FEB-2000; 2000WO-USG06811.
10-MAR-2000; 2000WO-USG06811.
11-MAR-2000; 2000WO-USG06811.
15-MAR-2000; 2000WO-USG0681.
15-MAR-2000; 2000WO-USG01358.
11-MAR-2000; 2000WO-USG1358.
11-MAY-2000; 2000WO-USG1358.
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13-MAY-2000; 2000WO-USG1358.
22-MAY-2000; 2000WO-USG1358.
23-JUN-2000; 2000WO-USG1358.
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                               98WO-US025108.
98US-0113296P.
99WO-US000106.
99WO-US005028.
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99US-0149336F.
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2000US-0213637P.
2000WO-US020710.
2000WO-US022031.
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99US-0158663P.
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                     98WO-US021141
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                                                                                              23 - TUN - 1999;
07 - JUL - 1999;
26 - JUL - 1999;
28 - JUL - 1999;
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15 - SEP - 1999;
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01-DEC-1998;
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08-MAR-1999;
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02-JUN-1999;
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Matches
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99WO-US028313. 99WO-US028301. 99WO-US028634. 99WO-US021090 99WO-US021547

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2000WO-US004414 2000WO-US004914

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2000WO-US007377

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01-DEC-1999;
01-DEC-1999;
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2000WO-US023328 2000WO-US032678

2000WO-US015264 2000WO-US020710 2000WO-US022031 :000WO-US023522 2000WO-US030952

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2001US-00941992 GETH) GENENTECH INC. 29-JUN-2001;

Eaton DL; rd A, Godowski PJ; Paoni NF; Wood WI; Baker KP, Botstein D, Desnoyers L, Eaton ng S, Gerber H, Gerritsen ME, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, Tt TA, Tumas D, Watenabe CK, Williams PM, Ferrara N, Fong S, Gerber H, Grimaldi JC, Gurney AL, Kljav Roy MA, Stewart TA, Tumas D, Ashkenazi AJ,

WPI; 2003-247083/24.

P-PSDB; ABU59174

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Claim 2; Fig 291; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in inhibiting a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO134 and PRO136 trimulate adrenal cortical capillary endothelial growth, and PRO136, PRO943, PRO926, PRO926, PRO926, PRO943, PRO926, PRO926, PRO1068 or PRO535, PRO826, PRO916, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO912 inhibits vascular calcing acancerous tumours. PRO912 inhibits vascular calcing acancerous tumours is proliferation of endothelial growth factor (VDEP) stimulated proliferation of endothelial which would be beneficial in inhibiting tumour growth. PRO926, PRO1068, PRO1364 and PRO1375 stimulate proliferation of stimulated T-1ymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1058 or PRO1132 enhance survival of

98US-0088025P. 98US-0088026P. 98US-0088028P. 98US-0088029P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
retinal neurons cells (PRO1132 is also enhances survival/proliferation of photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with nephropathies associated with dermatitis, herpetiformis or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and arthus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide
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04-AUG-1998; 04-AUG-1998; 04-AUG-1998; 10-AUG-1998; 110-AUG-1998; 111-AUG-1998; 117-AUG-1998; 118-AUG-1998; 2000WO-US005841. 2000WO-US006319. 2000WO-US006884.

22-DEC-1998; 28-DEC-1998; 08-MAR-1999; 08-MAR-1999; 12-MAR-1999; 07-JUL-1999; 20-JUL-1999; 20-JUL-1999; 17-MG-1999; 17-MG-1999; 17-MG-1999; 17-MG-1999; 17-MG-1999; 11-SEP-1999; 11-SEP-1999; 11-DEC-1999; 11-DEC-1999; 11-DEC-1999; 11-DEC-1999; 11-FEB-2000; 22-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 11-MAR-2000; 15-MAR-2000; 15-MAR-2000; 15-MAR-2000;

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30-MAY-2000; 2000W0-US014941.
28-JUL-2000; 2000W0-US015264.
28-JUL-2000; 2000W0-US022031.
23-AUG-2000; 2000W0-US02328.
24-AUG-2000; 2000W0-US03328.
08-NOV-2000; 2000W0-US03328.
28-FEB-2001; 2000W0-US031695.
01-JUN-2001; 2001W0-US011660.
29-JUN-2001; 2001W0-US0116692.
29-JUN-2001; 2001W0-US011666.
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15-WAY-2000; 2000WO-US013358.
17-WAY-2000; 2000WO-US013705.
22-WAY-2000; 2000WO-US014042.
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7. 3.2e-06; Indels
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                                                                                                                                                                                  Query Match
13.9%; Score 78; DB
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 78; Conservative 0; Mismatches
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20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013705.
17-MAY-2000; 2000WO-US013705.
30-MAY-2000; 2000WO-US014042.
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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive compensation and for modulating at least come biological activity of a cell. The PRO polypeptides or polymerlectides are also useful in gene therapy, in chromosome compensation, as chromosome markers, or in generating probes. The PRO identification, as chromosome markers for protein electrophoresis, polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or PRO, and in affinity purification of PRO from recombinant cell culture or matural sources. The sequences presented in ABX90083-ABX90468 are the contains, the primers amplifying and the probes detecting the PRO polymucleotides of the invention. Note: The sequence data for this patent of polymucleotides of the invention format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCTGCCCGCGC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGGAGCCGCAGGTTCCCGGGG 60
                                                         New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder; antibacterial; immunosuppressive; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%; Score 78; DB 7; Length 570; 100.0%; Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
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0; Mismatches
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                                                                                                                         Claim 2; Fig 289; 650pp; English.
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                        WPI; 2003-288106/28.
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                                        P-PSDB; ABU60604.
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13-NOV-1997;
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2000WO-US023522.
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2001US-00941992
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28-JUL-2000;
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23-AUG-2000;
24-AUG-2000;
08-NOV-2000;
01-DEC-2000;
28-FEB-2001;
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Godowski PJ; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godd Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paor Roy MA, Stewart IA, Tunas D, Watanabe CK, Williams PM, Woc Roy MA, Zhang Z;

WPI; 2003-102117/09. P-PSDB; ABU13986.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 289; 649pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, and for inconding PRO polypeptides are useful as hybridisation probes, in charmonic properties of cells expressing PRO polypeptides and for for chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of properties of chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the construct hybridisation probes for mapping the individuals with genetic disorders, in gene therapy, for chromosome chartication, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention. Note: The construct by the USPTO web site at sequence down/propried in electronic format directly from the USPTO web site at sequence government and response the properties of the invention.

Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

0; Gaps Length 570; 0; Indels DB 7; Le Query Match 13.9%; Score 78; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 78; Conservative 0; Mismatches δ

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534 GCCCCGAGCCCCCGCGCC 551

Search completed: June 6, 2004, 16:54:37 Job time : 406 secs Н

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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odel	June 6, 2004, 15:43:12 ; Search time 3796 Seconds (without alignments) 6428.379 Million cell updates/sec	SRQ19PLUS12 563 1 cggccggggaggcgggccgggcccgcgcccggggagg 563		95 residues	parameters: 6940544
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ALIGNMENTS

AC022095 127488 bp DNA linear HTG 20-APR-2001
13 unordered pieces.
14 unordered pieces.
NAC022095.
AC022095.5 GI:13699618
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens (condata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.

15 (Dases 1 to 127488)
16 (Dose Joint Genome Institute.
Sequencing of Human Chromosome 5 RESULT 1 AC022095/c LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE

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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 110477 bases at least Q40
Consensus quality: 11721 bases at least Q30
Consensus quality: 120225 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone="CTB-36B8"
/clone lib="CalTech human BAC library B"
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1216: gap of unknown length
2254: contig of 1038 bp in length
2354: gap of unknown length
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                              2 (bases 1 to 127488)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 78060
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Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgaller, B., Brown, A., Burkett, G., Campopiano, A., Castler, R., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Garden, S., Goytete, M., Grahm, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McDheeters, R., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McHord, C., Menga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, M., Pisani, C., Pollaraw, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
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1 (bases 1 to 168347)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 5, clone RP11-451H23

Unpublished
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Homo sapiens (human)
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contig of 12224 bp in length
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contig of 11671 bp in length
gap of 100 bp
contig of 14796 bp in length
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36 168347: contig of 11112 bp in length.
Location/Qualifiers
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/note="assembly_fragment"
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            Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 25, 2000 this sequence version replaced gi:7210017.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
  Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                       Center project name: 16686
Center clone name: 451 H 23
Center clone name: 451 H 23
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150422 bases at least Q40
Consensus quality: 155524 bases at least Q30
Consensus quality: 163013 bases at least Q20
Insert size: 16547; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                      Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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AC122714 190024 bp DNA linear PRI 04-MAR-2003 Homo sapiens chromosome 5 clone RPI1-451H23, complete sequence. AC122714

RESULT 3
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                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 190024)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Betimated Total Number of Errors is 0.9.
NOTS: Shatter libraries failed to verify the dinucleotide repeat
NOTS: Shatter libraries failed to verify the dinucleotide repeat
124370-125308. Unsure number of repeat copies
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-MAR-2003) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Mar 4, 2003 this sequence version replaced gi:21206277. Draft sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unsure number
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="NOTE: Shatter libraries failed to verify the
dinucleotide repeat region 124370-125308. Unsure num
of repeat copies 124370-125308. Forced join 124996."
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                                                            1 (bases 1 to 190024)
DOB Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
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308 Joint Genome Institute.
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81129 GGGGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCACGGCCGT 81070
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                                                                                                                                                                                                                                                                                                                                                                                                                        130129 bp DNA linear HTG 25-JAN-2002
Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
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DOE Joint Genome Institute.
DOE Joint Genome Institute.
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 130129)
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Consensus quality: 128011 bases at least Q30
Consensus quality: 128842 bases at least Q30
Consensus quality: 128842 bases at least Q30
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
                                                                                             31069 GAGCGGAGCGGGCAGGCTTTCTCAGGAGCGCGGGCGAGGCCGGGCGAGGCGTGAGGCGGAGG
                                                                                                                                                             480 ACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGGGGGCCCCG
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4420: gap of unknown length
23712: contig of 19220 bp in length
23812: gap of unknown length
48602: contig of 24790 bp in length
48702: gap of unknown length
130129: contig of 81427 bp in length.
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
HOmo sapiens (human)
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Sequencing of Human Chromosome
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Center: Joint Genome Institute
Center Code: JGI
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166777 bp DNA linear HTG 07-MAR-2002

Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (base 1 to 16(777)

DOB Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                          24569 CGGCCGGGGAGGCGCCCGGGAGTGAGCCTGATCGTCCCTGGCGCCTCCACCTCCCCAGG
                                                                                                                                                                                                                        61 CGCAGAAGGCGCCCAACGAGGACCCCCAGTGCCCGACGTTGCCACGGTCTGGGATCAGAGG
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                                                                                                                                                 1 CGGCCGGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCTGGCGCCTCCACCTCCCCAGG
                                                                                                                                                                                                                                                           CAGGGACCAGGGAGCCAGGAACTGCGCCGCCCCCCCCCTGCCCTGGCGCGAGGGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                      241 AGACCCCAAAGCGAAGGTGCGGGCCGGGGTGGGCCTCGCGGAGACAAAGGCCGGGCCTGC
                                                                                                               Gaps
                                                                        Length 130129;
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/clone="CTD-2013L15"
/clone_lib="CalTech human BAC library D"
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HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
                                                                        Score 478.8; DB 2;
Pred. No. 1.3e-70;
0; Mismatches 7;
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DOE Joint Genome Institute.
                                                                        Query Match
Best Local Similarity 95.3%;
Matches 522; Conservative
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360 GGGGCACGGGCTTC 119446 GGGGCACGGGCTTC 420 GAGCGGACGGGCA 119506 GAGCGGGTATAAGA 479 GACCGGGTATAAGA 119566 GACCGGGTATAAGA	7-AUG-2 lung. heophyt ; PACCA	Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroupe, S.D. TITLE Reagents and methods useful for detecting diseases of the lung JOURNAL Patent: JP 200152225-A 5 13-NOV-2001; ABECTI LABORATORIES COMMENT FN JP 2001522225-A/5 PD 13-NOV-2001 PR 31-JAN-1999 JP 1998533078 PR 31-JAN-1997 US 06/791710 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI PILLAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI	KLASS, PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHE PI STROUPE PC CL2N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers CC Topology: Linear; I. 562 Ource /organism="Zea mays" // Organism="Zea mays" // Mol_Lype="genomic DNA" // db_xref="taxon:4577"	ORIGIN Query Match Query Match Query Match Best Local Similarity 99.2%; Pred. No. 1.88-10; Length 562; Best Local Similarity 99.2%; Pred. No. 1.88-10; Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 431 GCAGGCTTTCTCAGAGGCGGGGGGGGGGGGGGGGGGGGG
TITLE Direct Submission JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON MAR 7, 2002 this sequence version replaced gi:18369924. COMMENT ON MAR 7, 2002 this sequence version replaced gi:18369924. Center: Joint Genome Institute Center Joint Genome Institute Center of the project Information Center Project Information Center Project Name: 1519801 Center Clone name: RPCI-11_58619	tristics puality: 163497 by puality: 166432 b) mustr size: 18625 msert size: 1665 erage: 9.4 in 0.7 forage: 10.5 in 0.7 forage	62338 62337; 62338 75837; 75838 166777; Location/Qu. 1. 166777 Accanism="/mol_type="//db_xref="//db_xref="//chromosome//clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="%plane"/clone="plane"/clon	Query Match B4.4%; Score 475; DB 2; Length 166777; Best Local Similarity 95.5%; Pred. No. 5.2e-70; Additional Similarity 3; Matches 528; Conservative 0; Mismatches 5; Indels 20; Gaps 3; Qy 119104 CGGCGGGGAGGCGGGAGTGAGCCTGATCGTCCTGGGGCTTCACCTCCCCAGG 119163 Qy 61 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCGACGTTGCCACGCTTGGGATCAGAGG 120 Db 119164 CGCAGAAGGCGCCCACGAGGACCCCCAGTGCCCCAGGTTGCCACGGTTGGGATCAGAGG 120 Db 119164 CGCAGAAAGGCGCCCACGAGGACCCCCAGTGCCCCAGGTTGCCACGGTTTGGGATCAGAGG 120	121 CAGGGACCAGGAACTGCGCCCCCCCCCCTGCCCTGGCGCAGGAAGCT

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60/094983 PR
2129 PI PREETI
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                                                                                                                                                                              PP 25-JUJ-2002
PP 25-JUJ-1999 UP 2000557363
PR 26-JUN-1999 US 60/094983 PR 26-JUN-1999 US 60/094983 PR 26-JUN-1999 US 60/103686, 11-DEC-1999 US 60/112129 PI PREETI LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER, PI MARIAH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE, PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN PC CIZNIS/09, AGIRS/00, AGIRS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
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A novel method of diagnosing, monitoring and staging lung cancer
Patent: JP 2002515262-A 6 28-MAY-2002;
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2P 2002515262-A/6
2B MAY-2002
12-MAY-1999 JP 2000549766
21-MAY-1999 US 60/086212
FEI YANG, ROBERTO A MACINA, YONGMING SUN
G12N15/09, C12201/68, G01N13/56, C12N15/00
A novel method of diagnosing, monitoring and staging lung
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     Yue, H., Patterson, C.,
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Baughn, M.R., Akerblom, I.E., Young, J.A., Reddy, R., Hillman, J.L. and Bandman, O. Human signal peptide-containing protein Patent: JP 20025;9030-A 65 02-JUL-2002; INCYTE PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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100.0%; Pred. No. 7.8e-0.
iive 0; Mismatches
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/db_xref="taxon:9606"
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JP 2002519030-A/65
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/organism="Homo
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JP 2002515262-A/6.
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Homo sapiens
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Matches 92, Conservative
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PR 21-MAY-15
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BD226775
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1 (bases 1 to 190)

S Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Rasaell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the lung patent: JP 200152225-A 1 13-NOV-2001;
PABOTT LABORATORIES
PN JP 2001522225-A/1

PD 13-NOV-2001

PP 30-JAN-1998 JP 1998533078

PR 31-JAN-1997 US 08/79110
                                                                                 BD082137 190 bp DNA linear PAT 27-AUG-2002 Reagents and methods useful for detecting diseases of the lung.
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PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
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Pred. No. 7.7e-10;
0; Mismatches 4;
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/mol_type="genomic_DNA"
/db_xxef="taxon:4577"
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JP 2002519030-A/65.
Homo sapiens (human)
Homo sapiens
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Sequence 407 from patent US 6478825.
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/db_xref="taxon:9606"
                                                  AX201348 569 bp
Sequence 27 from Patent W00153486.
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/organism="Homo sapiens"
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/wol_type="genomic DNA"
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AX201348.1 GI:15391167
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Topology: Linear;
Key
Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                     BDO82142 519 bp DNA linear PAT 27-AUG-2002 Reagents and methods useful for detecting diseases of the lung.
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Reagents and methods useful for detecting diseases of the lung Patent: JP 200152225-A 6 13-NOV-2001;

PN JP 200152225-A/6

PN JP 200152225-A/6

PP 30-JAN-1998 JP 1998533078

PR 31-JAN-1997 US 08/791710
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PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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0.0016;
hes 0; Indels
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                                                                                                                 16.3%; Score 92; DB 6; Le
.larity 100.0%; Pred. No. 7.8e-06;
Conservative 0; Mismatches 0;
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13.9%; Score 78; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 78; Conservative 0; Mismatches
                                                                                                                                                                                                                                                   520 CAGGITCCCCGCGCGCCCCGAGCCCCCGCGCCC
               1. .543
/organism="Homo sapiens"
/mol type="genomic DNA"
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/db_xref="taxon:4577"
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Location/Qualifiers
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JP 2001522225-A/6.
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PAT 30-AUG-2001
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Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,P.M., Watanabe,C.K. and Wood,W.I.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A Z 26-JUL-2001;
Genentech, Inc. (US)
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Unclassified.

1 (bases 1 to 570)
Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
Implant, method of making same and use of the implant for the treatment of bone defects

Treatment of bone defects

Patent: US 6478825-A.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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13.9%; Score 78; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 0;
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Sea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Subraryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 244)

Medel,P.A.B., Cohen,W., Colpitts,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodgres,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
Russell,J.C. and Strouge,S.D.
Reagents and methods useful for detecting diseases of the lung
Reagents and methods useful for detecting diseases of the lung
ABBOTT LABORATORIES

Py 200152225-A/2

Pp 30-JAN-1998 JP 1998533078

PR 31-JAN-1999 US 08/791710
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| translation="WILAALIGECVALSCSSAAAFIVGSAKRVAQPVAALKALIGALTV
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                               organism="Homo sapiens"
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                                                                                                                       1. .570
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79. .393
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                                                                                                                                                                                                                                                                     'product="SCGB3A1"
                                                                                                    /clone="DNA64884"
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JP 2001522225-A/2.
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1 (bases 1 to 570)

2 Clark.H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M. H., Yansura,D., Yi,S., Yu,G., Yunn,J., Zhang,M., Zhang,Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                   PAT 14-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY359064 570 bp mRNA linear PRI 03-OCT-2003 Homo sapiens clone DNA64884 SCGB3Al (UNQ629) mRNA, complete cds.
                                                                                                                                                                                                                                                                             Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kijavin, I., Napier, M.A., Pan, J., Paoni, N.Y., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 6; Length 5,0,0 Pred. No. 0.016;
                                                   linear
                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             the same
Patent: WO 0073454-A 407 07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13 (10), 2265-2270 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
13.9%; Score 78; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 78; Conservative 0; Mismatches
                                         Sequence 407 from Patent WO0073454. AX403520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genentech Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 GCCCCGAGCCCCCGCGCC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCCCCGAGCCCCCGCGCC 78
                                                                                                                   AX403520.1 GI:21437002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY359064.1 GI:37183245
                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                    DEFINITION
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ORGANISM
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RESULT 13
AX403520
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AY359064
LOCUS
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REFERENCE
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0; Gaps
Query Match 13.7%; Score 77; DB 6; Length 244; Best Local Similarity 98.7%; Pred. No. 0.003; Matches 77; Conservative 0; Mismatches 1; Indels
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474 GCGAGGACCGGGTAIAAGAAGCCICGGGCCCTGCCCGGGCAGCCGCAGGTTCCCCGCGC 533

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Search completed: June 6, 2004, 17:58:10 Job time: 3799 secs